

NOVEL PROTEIN AND METHODS FOR THE PRODUCTION OF THE NAME

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Abstract

A protein which inhibits osteoclast differentiation and/or maturation and a method of production of the protein. The protein is produced by human embryonic lung fibroblasts and has molecular weight of about 60 kD and about 120 kD under non-reducing conditions and about 60 kD under reducing conditions on SDS-polyacrylamide gel electrophoresis, respectively. The protein can be isolated and purified from culture medium of the said fibroblasts. Furthermore, the protein can be produced by gene engineering. The present invention includes cDNA for producing the protein by gene engineering, antibodies having specific affinity to the protein or a method for determination of the protein concentration using the antibodies.

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(57) A protein which inhibits osteoclast differentiation and/or maturation and a method of production of the protein. The protein is produced by human embryonic lung fibroblasts and has molecular weight of about 60 kD and about 120 kD under non-reducing conditions and about 60 kD under reducing conditions on SDS-polyacrylamide gel electrophoresis, respectively.

The protein can be isolated and purified from culture medium of the said fibroblasts. Furthermore, the protein can be produced by gene engineering.

The present invention includes cDNA for producing the protein by gene engineering, antibodies having specific affinity to the protein or a method for determination of the protein concentration using the antibodies.

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Description

Field of the invention

5 This invention relates to a novel protein, osteoclastogenesis inhibitory factor (OCIF), and methods for producing the protein.

Background of the invention

10 Human bones are always remodelling by the repeated process of resorption and reconstitution. In the process, osteoblasts and osteoclasts are considered to be the cells mainly responsible for bone formation and bone resorption, respectively. A typical example of disease caused by the progression of abnormal bone metabolism is osteoporosis. The disease is known to be provoked by the condition in which bone resorption by osteoclasts exceeds bone formation by osteoblasts, but the mechanism of osteoporosis has not yet been completely elucidated. Osteoporosis causes pain
15 in the bone and makes the bone fragile, leading to fracture. Since osteoporosis increases the number of bedridden old people, it has become a social issue with the increasing number of old people. Therefore, efficacious drugs for the treatment of the disease are expected to be developed. Bone mass reduction caused by the abnormal bone metabolism is thought to be prevented by inhibiting bone resorption, improving bone formation, or improving the balanced metabolism.

20 Bone formation is expected to be promoted by stimulating growth, differentiation, or activation of osteoblasts. Many cytokines are reported to stimulate growth or differentiation of osteoblasts, i.e. fibroblast growth factor (FGF) (Rodan S. B. et al., Endocrinology vol. 121, p1917, 1987), insulin-like growth factor-I (IGF-I) (Hock J.M. et al., Endocrinology vol. 122, p254, 1988), insulin-like growth factor-II (IGF-II) (McCarthy T. et al., Endocrinology vol. 124, p301, 1989), Activin A (Centrella M. et al., Mol. Cell. Biol. vol. 11, p250, 1991), Vasculotropin (Varonique M et al., Biochem. Biophys. Res. Commun. vol. 199, p380, 1994), and bone morphogenetic protein (BMP) (Yamaguchi, A et al., J. Cell Biol. vol. 113, p682, 1991, Sampath T.K. et al., J. Biol Chem. vol.267, p20532, 1992, and Knutsen R. et al., Biochem. Biophys. Res. Commun. vol.194, p1352, 1993).

On the other hand, cytokines which inhibits differentiation and/or maturation of osteoclasts have been paid attention and have been intensively studied. Transforming growth factor- β (Chenu C. et al., Proc. Natl. Acad. Sci. USA, vol.85, p5683, 1988) and interleukin-4 (Kasano K. et al., Bone-Miner., vol. 21, p179, 1993) are found to inhibit the differentiation of osteoclasts. Calcitonin (Bone-Miner., vol.17, p347, 1992), Macrophage colony-stimulating factor (Hattersley G. et al. J. Cell. Physiol. vol.137, p199, 1988), interleukin-4 (Watanabe, K. et al., Biochem. Biophys. Res. Commun. vol. 172, p1035, 1990), and interferon- γ (Gowen M. et al., J. Bone Miner. Res., vol.1, p469, 1986) are found to inhibit bone resorption by osteoclasts.
30

35 These cytokines are expected to be efficacious drugs for improving bone mass reduction by stimulating bone formation and/or by inhibiting bone resorption. The cytokines such as insulin like growth factor-I and bone morphogenetic proteins are now investigated in clinical trials for their effects in treatment of patients with bone diseases. Calcitonin is already used as a drug to care osteoporosis and to diminish pain in osteoporosis.

40 Examples of drugs now clinically utilized for the treatment of bone diseases and for shortening the treatment period are dihydroxyvitamine D₃, vitamin K₂, calcitonin and its derivatives, hormones such as estradiol, ipriflavon, and calcium preparations. However, these drugs do not provide satisfactory therapeutic effects, and novel drug substances have been expected to be developed. As mentioned, bone metabolism is controlled in the balance between bone resorption and bone formation. Therefore, cytokines which inhibit osteoclast differentiation and/or maturation are expected to be developed as drugs for the treatment of bone diseases such as osteoporosis.

Disclosure of Invention

This invention was initiated from the view point described above. The purpose of this invention is to offer both a novel factor termed osteoclastogenesis inhibitory factor (OCIF) and a procedure to produce the factor efficiently.

50 The inventors have intensively searched for osteoclastogenesis inhibitory factors in human embryonic fibroblast IMR-90 (ATCC CCL186) conditioned medium and have found a novel osteoclastogenesis inhibitory factor (OCIF) which inhibits differentiation and/or maturation of osteoclasts.

The inventors have established a method for accumulating the protein to a high concentration by culturing IMR-90 cells using alumina ceramic pieces as the cell adherence matrices.

55 The inventors have also established an efficient method for isolating the protein, OCIF, from the IMR-90 conditioned medium using the following sequential column chromatography, ion-exchange, heparin affinity, cibacron-blue affinity, and reverse phase.

The inventors, based on the amino acid sequence of the purified natural OCIF, successfully cloned a cDNA encod-

ing this protein. The inventors established also a procedure to produce this protein which inhibits differentiation of osteoclasts. This invention concerns a protein which is produced by human lung fibroblast cells, has molecular weights in SDS-PAGE of 60 KD in the reducing conditions and 120 KD under the non-reducing conditions, has affinity for both cation-exchange resins and heparin, reduces its activity to inhibit differentiation and maturation of osteoclasts if treated for 10 minutes at 70 °C or for 30 minutes at 56 °C, and lose its activity to inhibit differentiation and maturation of osteoclasts by the treatment for 10 minutes at 90 °C. The amino acid sequence of the protein OCIF which is described in the present invention is clearly different from any of known factors inhibiting formation of osteoclasts.

The invention includes a method to purify OCIF protein, comprising : (1) culturing human fibroblasts, (2) applying the conditioned medium to a heparin column to obtain the adsorbed fraction, (3) purifying the OCIF protein using a cation-exchange column, (4) purifying the OCIF protein using a heparin affinity column, (5) purifying the OCIF protein using a Cibacron blue affinity column, (6) isolating the OCIF protein using reverse-phase column chromatography. Cibacron blue F3GA coupled to a carrier made of synthetic hydrophilic polymers is an example of materials used to prepare Cibacron blue columns. These columns are conventionally called "blue columns".

The invention includes a method for accumulating the OCIF protein to a high concentration by culturing human fibroblasts using alumina ceramic pieces as the cell-adherence matrices.

Moreover, the inventors determined the amino acid sequences of the peptides derived from OCIF, designed the primers based on these amino acid sequences, and obtained cDNA fragments encoding OCIF from a cDNA library of IMR-90 cells.

20 Detailed description of the invention

The OCIF protein of the present invention can be isolated from human fibroblast conditioned medium with high yield. The procedure to isolate OCIF is based on ordinary techniques for purifying proteins from biomaterials, in accordance with the physical and chemical properties of OCIF protein. For example, concentrating procedure includes ordinary biochemical techniques such as ultrafiltration, lyophilization, and dialysis. Purifying procedure includes combinations of several chromatographic techniques for purifying proteins such as ion-exchange column chromatography, affinity column chromatography, gel filtration column chromatography, hydrophobic column chromatography, reverse phase column chromatography, and preparative gel electrophoresis. The human fibroblast used for production of the OCIF protein is preferably IMR-90. A method for producing the IMR-90 conditioned medium is preferably a process comprising, adhering human embryonic fibroblast IMR-90 cells to alumina ceramic pieces in roller-bottles, using DMEM medium supplemented with 5 % new born calf serum for the cell culture, and cultivating the cells in roller-bottles for 7 to 10 days by stand cultivation. CHAPS (3-[(3-cholamid opropyl)-dimethylammonio]-1-propanesulfonate) is preferably added to the buffer as a detergent in the purification steps of OCIF protein.

OCIF protein of the instant invention can be initially obtained as a heparin binding basic OCIF fraction by applying the culture medium to a heparin column (Heparin-Sepharose CL-6B, Pharmacia), eluting with 10 mM Tris-HCl buffer, pH 7.5, containing 2 M NaCl, and then by applying the OCIF fraction to a Q⁻ anion-exchange column (HiLoad-Q/FF, Pharmacia), and collecting non-adsorbed fraction. OCIF protein can be purified by subjecting the obtained OCIF fraction to purification on a S⁺ cation-exchange column (HiLoad-S/FF, Pharmacia), a heparin column (Heparin-5PW, TOSOH), Cibacron Blue column (Blue-5PW, TOSOH), and a reverse-phase column (BU-300 C4, Perkin Elmer) and the material is defined by the previously described properties.

The present invention relates to a method of cloning cDNA encoding the OCIF protein based on the amino acid sequence of natural OCIF and a method of obtaining recombinant OCIF protein that inhibits differentiation and/or maturation of osteoclasts. The OCIF protein is purified according to the method described in the present invention and is treated with endopeptidase (for example, lysylendopeptidase). The amino acid sequences of the peptides produced by the digestion are determined and the mixture of oligonucleotides that can encode each internal amino acid sequence was synthesized. The OCIF cDNA fragment is obtained by PCR (preferably RT-PCR, reverse transcriptase PCR) using the oligonucleotide mixtures described above as primers. The full length OCIF cDNA encoding the OCIF protein is cloned from a cDNA library using the obtained OCIF DNA fragment as a probe. The OCIF cDNA containing the entire coding region is inserted into an expression vector. The recombinant OCIF can be produced by expressing the OCIF cDNA containing the entire coding region in mammalian cells or bacteria.

The present invention relates to the novel proteins OCIF2, OCIF3, OCIF4, and OCIF5 that are variants of OCIF and have the activity described above. These OCIF variants are obtained from the cDNA library constructed with IMR-90 poly(A)⁺ RNA by hybridization using the OCIF cDNA fragment as a probe. Each of the OCIF variant cDNAs containing the entire coding region is inserted into an expression vector. Each recombinant OCIF variant can be produced by expressing each of the OCIF variant cDNAs containing the entire coding region in the conventional hosts. Each recombinant OCIF variant can be purified according to the method described in this invention. Each recombinant OCIF variant has an ability to inhibit osteoclastogenesis.

The present invention further includes OCIF mutants. They are substitution mutants comprising replacement of one

lane 15 ; molecular weight marker proteins
 lane 16 ; a monomer type nOCIF protein
 lane 17 ; a dimer type nOCIF protein
 lane 18 ; a monomer type rOCIF(E) protein
 lane 19 ; a dimer type rOCIF(E) protein
 lane 20 ; a monomer type rOCIF(C) protein
 lane 21 ; a dimer type rOCIF(C) protein

Figure 9 shows comparison of amino acid sequences between OCIF and OCIF2.

Figure 10 shows comparison of amino acid sequences between OCIF and OCIF3.

Figure 11 shows comparison of amino acid sequences between OCIF and OCIF4.

Figure 12 shows comparison of amino acid sequences between OCIF and OCIF5.

Figure 13 shows standard curve for determination of OCIF protein concentration by an EIA employing anti-OCIF polyclonal antibodies.

Figure 14 shows standard curve for determination of OCIF protein concentration by an EIA employing anti-OCIF monoclonal antibodies.

Figure 15 shows the effect of rOCIF protein on osteoporosis.

Best Mode for Carrying Out the Invention

The present invention will be further explained by the following examples, however, the scope of the invention is not restricted to the examples.

EXAMPLE 1

Preparation of a conditioned medium of human fibroblast IMR-90

Human fetal lung fibroblast IMR-90 (ATCC-CCL186) cells were cultured on alumina ceramic pieces (80 g) (alumina: 99.5%, manufactured by Toshiba Ceramic K.K.) in DMEM medium (manufactured by Gibco BRL Co.) supplemented with 5% CS and 10mM HEPES buffer (500 ml/roller bottle) at 37°C under the presence of 5% CO₂ for 7 to 10 days using 60 roller bottles (490 cm², 110 x 171mm, manufactured by Coning Co.) in static culture. The conditioned medium was harvested, and a fresh medium was added to the roller bottles. About 30L of IMR-90 conditioned medium per batch culture was obtained. The conditioned medium was designated as sample 1.

EXAMPLE 2

Assay method for osteoclast development inhibitory activity

Osteoclast development inhibitory activity was assayed by measuring tartrate-resistant acid phosphatase (TRAP) activity according to the methods of M. Kumegawa et.al (Protein · Nucleic Acid · Enzyme, vol.34 p999, 1989) and N. Takahashi et.al (Endocrinology, vol.122, p1373, 1988) with modifications. Briefly, bone marrow cells obtained from 17 day-old mouse were suspended in α -MEM (manufactured by GIBCO BRL Co.) containing 10% FBS, 2x10⁻⁸M of activated vitamin D₃, and each test sample, and were inoculated to each well of 96-well plate at a cell density of 3x10⁵ cells/0.2 ml/well. The plates were incubated for 7 days at 37°C in humidified 5%CO₂. Cultures were further continued by replacing 0.16 ml of old medium with the same volume of fresh medium on day 3 and day 5 after starting cultivation. On day 7, after washing the plates with phosphate buffered saline, cells were fixed with ethanol/acetone (1:1) for 1 min. at room temperature, and then osteoclast development was tested by determining for phosphatase activity using a kit (Acid Phosphatase, Leucocyte, Catalog No. 387-A, manufactured by Sigma Co.). The decrease of TRAP positive cells was taken as an indication of OCIF activity.

EXAMPLE 3

Purification of OCIF

i) Heparin Sepharose CL-6B column chromatography

The 90L of IMR-90 conditioned medium (sample 1) was filtrated with 0.22 μ membrane filter (hydrophilic Milidisk, 2000 cm², Milipore Co.), and was divided into three portions. Each portion (30 l) was applied to a heparin Sepharose

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CL-6B column (5 x 4.1 cm, Pharmacia Co.) equilibrated with 10mM Tris-HCl containing 0.3M NaCl, pH 7.5. After washing the column with 10mM Tris-HCl, pH 7.5 at a flow rate of 500 ml/hr., heparin Sepharose CL-6B adsorbent protein fraction was eluted with 10mM Tris-HCl, pH 7.5, containing 2M NaCl. The fraction was designated as sample 2.

5 ii) HiLoad-Q/FF column chromatography

The heparin Sepharose-adsorbent fraction (sample 2) was dialyzed against 10mM Tris-HCl, pH 7.5, supplemented with CHAPS to a final concentration of 0.1%, incubated at 4 °C overnight, and divided into two portions. Each portion was then applied to an anion-exchange column (HiLoad-Q/FF, 2.6 x 10 cm, Pharmacia Co.) which was equilibrated with 10 50mM Tris-HCl, 0.1% CHAPS, pH 7.5 to obtain a non-adsorbent fraction (1000 ml). The fraction was designated as sample 3.

iii) HiLoad-S/HP column chromatography

15 The HiLoad-Q non-adsorbent fraction (sample 3) was applied to a cation-exchange column (HiLoad-S/HP, 2.6 x 10 cm, Pharmacia Co.) which was equilibrated with 50 mM Tris-HCl, 0.1% CHAPS, pH 7.5. After washing the column with 50 mM Tris-HCl, 0.1% CHAPS, pH 7.5, the adsorbed protein was eluted with linear gradient from 0 to 1 M NaCl at a flow rate of 8 ml/min for 100 min. and fractions (12 ml) were collected. Each ten fractions from number 1 to 40 was pooled to form one portion. Each 100 µl of the four portions was tested for OCIF activity. OCIF activity was observed in 20 fractions from 11 to 30 (as shown in Figure 1). The fractions from 21 to 30 which had higher specific activity were collected and was designated as sample 4.

iv) Heparin-5PW affinity column chromatography

25 One hundred and twenty ml of HiLoad-S fraction from 21 to 30 (sample 4) was diluted with 240 ml of 50 mM Tris-HCl, 0.1% CHAPS, pH 7.5, and applied to heparin-5PW affinity column (0.8 x 7.5 cm, Tosoh Co.) which was equilibrated with 50mM Tris-HCl, 0.1% CHAPS, pH 7.5. After washing the column with 50mM Tris-HCl, 0.1% CHAPS, pH 7.5, the adsorbed protein was eluted with linear gradient from 0 to 2M NaCl at a flow rate of 0.5ml/min for 60 min. and fractions (0.5 ml) were collected. Fifty µl was removed from each fraction to test for OCIF activity. The active fractions, 30 eluted with 0.7 to 1.3M NaCl was pooled and was designated as sample 5.

v) Blue 5PW affinity column chromatography

35 Ten ml of sample 5 was diluted with 190 ml of 50mM Tris-HCl, 0.1% CHAPS, pH 7.5 and applied to a blue-5PW affinity column, (0.5x5 cm, Tosoh Co.) which was equilibrated with 50mM Tris-HCl, 0.1% CHAPS, pH 7.5. After washing the column with 50mM Tris-HCl, 0.1% CHAPS, pH 7.5, the adsorbed protein was eluted with a 30 ml linear gradient from 0 to 2M NaCl at a flow rate of 0.5 ml/min., and fractions (0.5 ml) were collected. Using 25 µl of each fraction, OCIF activity was evaluated. The fractions number 49 to 70, eluted with 1.0-1.6M NaCl had OCIF activity.

40 vi) Reverse phase column chromatography

The blue 5PW fraction obtained by collecting fractions from 49 to 50 was acidified with 10µl of 25% TFA and applied to a reverse phase C4 column (BU-300, 2.1x220mm, manufactured by Perkin-Elmer) which was equilibrated with 0.1% of TFA and 25% of acetonitrile. The adsorbed protein was eluted with linear gradient from 25 to 55% acetonitrile at a 45 flow rate of 0.2 ml/min. for 60 min., and each protein peak was collected (Fig.3). One hundred µl of each peak fraction was tested for OCIF activity, and peak 6 and the peak 7 had OCIF activity. The result was shown in Table 1.

50

55

Table 1

OCIF activity eluted from reverse phase C4 column				
Sample	Dilution			
	1/40	1/120	1/360	1/1080
Peak 6	++	++	+	-
Peak 7	++	+	-	-
[++ means OCIF activity inhibiting osteoclast development more than 80%, + means OCIF activity inhibiting osteoclast development between 30% and 80%, and - means no OCIF activity.]				

EXAMPLE 4

Molecular weight of OCIF protein

The two protein peaks (6 and 7) with OCIF activity were subjected to SDS-polyacrylamide gel electrophoresis under reducing and non-reducing conditions. Briefly, 20 μ l of each peak fraction was concentrated under vacuum and dissolved in 1.5 μ l of 10mM Tris-HCl, pH 8, 1mM EDTA, 2.5% SDS, 0.01% bromophenol blue, and incubated at 37°C overnight under non-reducing conditions or under reducing conditions (with 5% of 2-mercaptoethanol). Each 1.0 μ l of sample was then analyzed by SDS-polyacrylamide gel electrophoresis with a gradient gel of 10-15% acrylamide (Pharmacia Co.) and an electrophoresis-device (Fast System, Pharmacia Co.). The following molecular weight marker proteins were used to calculate molecular weight : phosphorylase b (94 kD), bovine serum albumin (67 kD), ovalbumin (43 kD), carbonic anhydrase (30 kD), trypsin inhibitor (20.0 kD), and lactalbumin (14.4 kD). After electrophoresis, protein bands were visualized by silver stain using Phast Silver Stain Kit. The results were shown in Fig. 4.

A protein band with an apparent 60 KD was detected in the peak 6 protein under both reducing and non-reducing conditions. A protein band with an apparent 60 KD was detected under reducing conditions and a protein band with an apparent 120 KD was detected under non-reducing conditions in the peak 7 protein. Therefore, the protein of peak 7 was considered to be a homodimer of the protein of peak 6.

EXAMPLE 5

Thermostability of OCIF

Twenty μ l of sample from the blue-5PW fractions 51 and 52 was diluted to 30 μ l with 10 mM phosphate buffered saline, pH 7.2, and incubated for 10 min. at 70°C or 90 °C, or for 30 min. at 56°C. The heat-treated samples were tested for OCIF activity. The results were shown in Table 2.

Table 2

Thermostability of OCIF			
Sample	Dilution		
	1/300	1/900	1/2700
untreated	++	+	-
70°C, 10 min	+	-	-
56°C, 30 min	+	-	-
90°C, 10 min	-	-	-
[++ means OCIF activity inhibiting osteoclast development more than 80%, +means OCIF activity inhibiting osteoclast development between 30% and 80%, and - means no OCIF activity.]			

EXAMPLE 6

Internal amino acid sequence of OCIF protein

Each 2 fractions (1 ml) from No. 51-70 of blue-5PW fraction was acidified with 10 μ l of 25% TFA, and was applied to a reverse phase C4 column (BU-300, 2.1x220mm, manufactured by Perkin-Elmer Co.) equilibrated with 25% of acetonitrile containing 0.1 % TFA. The adsorbed protein was eluted with a 12 ml linear gradient of 25 to 55% acetonitrile at a flow rate of 0.2 ml/min, and the protein fractions corresponding to peak 6 and peak 7 were collected, respectively. The protein of each peak was applied to a protein sequencer (PROCISE 494, Perkin-Elmer Co.). However, the N-terminal sequence of the protein of each peak could not be analyzed. Therefore, N-terminal of the protein of each peak was considered to be blocked. So, internal amino acid sequences of these proteins were analyzed.

The protein of peak 6 or peak 7 purified by C4-HPLC was concentrated by centrifugation and pyridylethylated under reducing conditions. Briefly, 50 μ l of 0.5 M Tris-HCl, pH 8.5, containing 100 μ g of dithiothreitol, 10mM EDTA, 7 M guanidine-HCl, and 1% CHAPS was added to each samples, and the mixture was incubated overnight in the dark at a room temperature. Each the mixture was acidified with 25% TFA (a final concentration 0.1%) and was applied to a reversed phase C4 column (BU-300, 2.1x30mm, Perkin-Elmer Co.) equilibrated with 20 % acetonitrile containing 0.1 % TFA. The pyridil-ethylated OCIF protein was eluted with a 9 ml linear gradient from 20 to 50% acetonitrile at a flow rate of 0.3 ml/min, and each protein peak was collected. The pyridil-ethyated OCIF protein was concentrated under vacuum, and dissolved in 25 μ l of 0.1 M Tris-HCl, pH 9, containing 8 M Urea, and 0.1 % Tween 80. Seventy three μ l of 0.1 M Tris-HCl, pH 9, and 0.02 μ g of lysyl endopeptidase (Wako Pure Chemical, Japan) were added to the tube, and incubated at 37 °C for 15 hours. Each digest was acidified with 1 μ l of 25% TFA and was applied to a reverse phase C8 column (RP-300, 2.1x220mm, Perkin-Elmer Co.) equilibrated with 0.1% TFA.

The peptide fragments were eluted from the column with linear gradient from 0 to 50 % acetonitrile at a flow rate of 0.2 ml/min for 70 min., and each peptide peak was collected. Each peptide fragment (P1 - P3) was applied to the protein sequencer. The sequences of the peptides were shown in Sequence Numbers 1 - 3, respectively.

EXAMPLE 7

Determination of nucleotide sequence of the OCIF cDNA

i) Isolation of poly(A) + RNA from IMR-90 cells

About 10 ug of poly(A) + RNA was isolated from 1x10⁸ cells of IMR-90 by using Fast Track mRNA isolation kit (Invitrogen) according to the manufacturer's instructions.

ii) Preparation of mixed primers

The following two mixed primers were synthesized based on the amino acid sequences of two peptides (peptide P2 and peptide P3, sequence numbers 2 and 3, respectively). All the oligonucleotides in the mixed primers No. 2F can code for the amino acid sequence from the sixth residue, glutamine (Gln) to the twelfth residue, leucine (Leu), in peptide P2. All the oligonucleotides in the mixed primers No. 3R can code for the amino acid sequence from the sixth residue, histidine (His), to the twelfth residue, lysine (Lys), in peptide P3. The sequences of the mixed primers No. 2F and No. 3R were shown in Table 3.

Table 3

No. 2F

5' -CAAGAACAAA CTTTCAATT-3'

G G G C C GC

A

G

No. 3R

5' -TTTATACATT GTAAAAGAAT G-3'

C G C G GCTG

A C

G T

iii) Amplification of OCIF cDNA fragment by PCR (Polymerase chain reaction)

First strand cDNA was generated using Superscript II cDNA synthesis kit (Gibco BRL) and 1 ug of poly (A) + RNA obtained in the example 7-i) according to the manufacturer's instructions. The DNA fragment encoding OCIF was obtained by PCR using the cDNA template and the primers shown in EXAMPLE 7-ii).

PCR was performed with the conditions as follows;

10X Ex Taq Buffer (Takara Shuzo)	5 ul
2.5 mM solution of dNTPs	4 ul
cDNA solution	1 ul
Ex Taq (Takara Shuzo)	0.25 ul
sterile distilled water	29.75 ul
40 uM solution of primers No. 2F	5 ul
40 uM solution of primers No. 3R	5 ul

The components of the reaction were mixed in a microcentrifuge tube. An initial denaturation step at 95 °C for 3 min was followed by 30 cycles of denaturation at 95°C for 30 sec annealing at 50 °C for 30 sec and extension at 70 °C for 2min. After the amplification, final extension step was performed at 70 °C for 5min. The size of PCR products were determined on a 1.5 % agarose gel electrophoresis. About 400 bp OCIF DNA fragment was obtained.

EXAMPLE 8

Cloning of the OCIF cDNA fragment amplified by PCR and determination of its DNA sequence

5 The OCIF cDNA fragment amplified by PCR in EXAMPLE 7-iii) was inserted in the plasmid, pBluescript II SK⁺ using DNA ligation kit ver. 2 (Takara Shuzo) according to the method by Marchuk, D. et al. (Nucleic Acids Res., vol 19, p1154, 1991). E.coli DH5 α (Gibco BRL) was transformed with ligation mixture. The transformants were grown and a plasmid containing the OCIF cDNA (about 400 bp) was purified using the commonly used method. This plasmid was called pBSOCIF. The sequence of OCIF cDNA in pBSOCIF was determined using Taq Dye Deoxy Terminator Cycle Sequencing kit (Perkin Elmer). The size of the OCIF cDNA is 397 bp. The OCIF cDNA encodes an amino acid sequence containing 132 residues. The amino acid sequences of the internal peptides (peptide P2 and peptide P3, sequence number 2 and 3, respectively) that were used to design the primers were found at N- or C- terminal side in the amino acid sequence of the 132 amino acid polypeptide predicted by the 397 bp OCIF cDNA. In addition, the amino acid sequence of the internal peptide P1 (sequence number 1) was also found in the predicted amino acid sequence of the polypeptide. These data show that the 397 bp OCIF cDNA is a portion of the full length OCIF cDNA.

EXAMPLE 9

Preparation of the DNA probe

20 The 397 bp OCIF cDNA was prepared according to the conditions described in EXAMPLE 7-iii). The OCIF cDNA was subjected to a preparative agarose gel electrophoresis. The OCIF cDNA was purified from the gel using QIAEX gel extraction kit (QIAGEN), labeled with [α^{32} P]dCTP using Megaprime DNA labeling system (Amersham) and used to select a phage containing the full length OCIF cDNA.

EXAMPLE 10

Preparation of the cDNA library

30 cDNA was generated using Great Lengths cDNA synthesis kit (Clontech), oligo (dT) primer, [α^{32} P]dCTP and 2.5 μ g of poly(A) + RNA obtained in the example 7-i) according to the manufacturer's instructions. EcoRI-Sall-NotI adaptor was ligated to the cDNA. The cDNA was separated from the free adaptor and unincorporated free [α^{32} P]dCTP. The purified cDNA was precipitated with ethanol and dissolved in 10 μ l of TE buffer (10 mM Tris-HCl (pH8.0), 1 mM EDTA). The cDNA with the adaptor was inserted in λ ZAP EXPRESS vector (Stratagene) at EcoRI site. The recombinant λ ZAP EXPRESS phage DNA containing the cDNA was in vitro packaged using Gigapack gold II packaging extract (Stratagene) and recombinant λ ZAP EXPRESS phage library was prepared.

EXAMPLE 11

40 Screening of recombinant phage

Recombinant phages obtained in EXAMPLE 10 were infected to E. Coli, XL1-Blue MRF⁺ (Stratagene) at 37 °C for 15 min.. The infected E.coli cells were added to NZY medium containing 0.7 % agar at 50°C and plated on the NZY agar plates. After the plates were incubated at 37 °C overnight, Hybond N (Amersham) were placed on the surface of plates containing plaques. The membranes were denatured in the alkali solution, neutralized, and washed in 2xSSC according to the standard protocol. The phage DNA was immobilized on the membranes using UV Crosslink (Stratagene). The membranes were incubated in the hybridization buffer (Amersham) containing 100 μ g/ml salmon sperm DNA at 65°C for 4 hours and then incubated at 65 °C overnight in the same buffer containing 2x10⁵ cpm/ml denatured OCIF DNA probe. The membranes were washed twice with 2xSSC and twice with a solution containing 0.1xSSC and 0.1 % SDS at 65 °C for 10 min each time. The positive clones were purified by repeating the screening twice. The purified λ ZAP EXPRESS phage clone containing about 1.6 kb DNA insert was used in the experiments described below. This phage was called λ OCIF. The purified λ OCIF and the infected into E. Coli XL1-Blue MRF⁺ (Stratagene) according to a protocol of λ ZAP EXPRESS cloning kit (Stratagene). The culture broth of infected XL1-Blue MRF⁺ was prepared. Purified 1OCIF and ExAssist helper phage (Stratagene) were co-infected into E. coli strain XL-1 blue MRF⁺ according to the protocol supplied with the kit. The culture broth of the co-infected XL-1 blue MRF⁺ was added to a culture of E. coli strain XLOR (Stratagene) to transform them. Thus we obtained a Kanamycin-resistant transformant harboring a plasmid designated pBKOCIF which is a pBKCMV (Stratagene) vector containing the 1.6 kb insert fragment. The transformant including the plasmid containing about 1.6 kb OCIF cDNA was obtained by picking up the kanamycin-

resistant colonies. The plasmid was called pBKOCIF. The transformant has been deposited to National Institute of Bio-science and Human-Technology (NIBH), Agency of Industrial Science and Technology as "FERM BP-5267" as pBK/O1F10. A national deposit (Accession number, FERM P-14998) was transferred to the international deposit, on October 25, 1995 according to the Budapest treaty. The transformant pBK/O1F10 was grown and the plasmid pBKOCIF was purified according to the standard protocol.

EXAMPLE 12

Determination of the nucleotide sequence of OCIF cDNA containing the full coding region.

The nucleotide sequence of OCIF cDNA obtained in EXAMPLE 11 was determined using Taq Dye Deoxy Terminator Cycle Sequencing kit (Perkin Elmer). The primers used were T3, T7 primers (Stratagene) and synthetic primers designed according to the OCIF cDNA sequence. The sequences of these primers are shown in sequence numbers 16 to 29. The nucleotide sequence of the OCIF cDNA is shown in sequence number 6 and the amino acid sequence predicted by the cDNA sequence is shown in sequence number 5.

EXAMPLE 13

Production of recombinant OCIF by 293/EBNA cells

i) Construction of the plasmid for expressing OCIF cDNA

pBKOCIF containing about 1.6 kb OCIF cDNA was prepared as described in EXAMPLE 11, and digested with restriction enzymes, BamHI and XhoI. The OCIF cDNA insert was cut out, separated by an agarose gel electrophoresis, and purified using QIAEX gel extraction kit (QIAGEN). The purified OCIF cDNA insert was ligated using DNA ligation kit ver. 2 (Takara Shuzo) to the expression vector pCEP4 (Invitrogen) digested with restriction enzymes, BamHI and XhoI. E.coli. DH5 α (Gibco BRL) was transformed with the ligation mixture. The transformants were grown and the plasmid containing the OCIF cDNA (about 1.6 kb) was purified using QIAGEN column (QIAGEN). The expression plasmid pCEPOCIF was precipitated with ethanol, and dissolved in sterile distilled water was used in the experiments described below.

ii) Transient expression of OCIF cDNA and analysis of the biological activity

Recombinant OCIF was produced using the expression plasmid, pCEPOCIF prepared in EXAMPLE 13-i) according to the method described below. 8×10^5 cells of 293/EBNA (Invitrogen) were inoculated in each well of the 6-well plate using IMDM containing 10 % fetal calf serum (Gibco BRL). After the cells were incubated for 24 hours, the culture medium was removed and the cells were washed with serum free IMDM. The expression plasmid, pCEPOCIF and lipofectamine (Gibco BRL) were diluted with OPTI-MEM (Gibco BRL) and were mixed, and added to the cells in each well according to the manufacture's instructions. Three μ g of pCEPOCIF and 12 μ l of lipofectamine were used for each transfection. After the cells were incubated with pCEPOCIF and lipofectamine for 38 hours, the medium was replaced with 1 ml of OPTI-MEM. After the transfected cells were incubated for 30 hours, the conditioned medium was harvested and used for the biological assay. The biological activity of OCIF was analysed according to the method described below. Bone marrow cells obtained from mice, 17 days-old, were suspended in α -MEM (manufactured by GIBCO BRL Co.) containing 10% FBS, 2×10^{-8} M activated vitamin D₃, and each test sample, and were inoculated and cultured for 7 days at 37°C in humidified 5%CO₂ as described in EXAMPLE 2. During incubation, 160 μ l of old medium in each well was replaced with the same volume of the fresh medium containing test sample diluted with 1×10^{-8} M of activated vitamin D₃ and α -MEM containing FBS on day 3 and day 5. On day 7, after washing the wells with phosphate buffered saline, cells were fixed with ethanol/acetone (1:1) for 1 min. and then osteoclast development was tested using acid phosphatase activity measuring kit (Acid Phosphatase, Leucocyte, Catalog No. 387-A, Sigma Co.). The decrease of the number of TRAP positive cells was taken as an OCIF activity. As result, the conditioned medium showed the same OCIF activity as natural OCIF protein from IMR-90 conditioned medium (Table 4).

Table 4

OCIF activity of 293/EBNA conditioned medium.							
Cultured Cell	Dilution						
	1/20	1/40	1/80	1/160	1/320	1/640	1/1280
OCIF expression vector transfected	++	++	++	++	++	+	-
vector transfected	-	-	-	-	-	-	-
untreated	-	-	-	-	-	-	-
[++ ; OCIF activity inhibiting osteoclast development more than 80%, + ; OCIF activity inhibiting osteoclast development between 30% and 80%, and - ; no OCIF activity.]							

iii) Isolation of recombinant OCIF protein from 293/EBNA-conditioned medium

293/EBNA-conditioned medium (1.8 l) obtained by cultivating the cells described in example 13-ii) was supplemented with 0.1 % of CHAPS and filtrated with 0.22 μ m membrane filter (Steribecs GS, Milipore Co.). The conditioned medium was applied to 50 ml of a heparin Sepharose CL-6B column (2.6 x 10 cm, Pharmacia Co.) equilibrated with 10mM Tris-HCl, pH 7.5. After washing the column with 10mM Tris-HCl, pH 7.5, the adsorbed protein was eluted from the column with linear gradient from 0 to 2 M NaCl at a flow rate of 4 ml/min for 100 min. and fractions (8 ml) were collected. Using 150 μ l of each fraction, OCIF activity was assayed according to the method described in EXAMPLE 2. OCIF active fraction (112 ml) eluted with approximately 0.6 to 1.2 M NaCl was obtained.

One hundred twelve ml of the active fraction was diluted to 1000 ml with 10 mM Tris-HCl, 0.1% CHAPS, pH 7.5, and applied to a heparin affinity column (heparin-5PW, 0.8 x 7.5 cm, Tosoh Co.) equilibrated with 10mM Tris-HCl, 0.1% CHAPS, pH 7.5. After washing the column with 10mM Tris-HCl, 0.1% CHAPS, pH 7.5, the adsorbed protein was eluted from the column with linear gradient from 0 to 2 M NaCl at a flow rate of 0.5ml/min for 60 min., and fractions (0.5 ml) were collected. Four μ l of each fraction was analyzed by SDS-polyacrylamide gel electrophoresis under reducing and non-reducing conditions as described in EXAMPLE 4. On SDS-PAGE under reducing conditions, a single band of rOCIF protein with an apparent 60 KD was detected in fractions from 30 to 32, under non-reducing conditions, bands of rOCIF protein with an apparent 60 KD and 120 KD were also detected in fractions from 30 to 32. The isolated rOCIF fraction from 30 to 32 was designated as recombinant OCIF derived from 293/EBNA (rOCIF(E)). 1.5 ml of the rOCIF(E) (535 μ g/ml) was obtained when determined by the method of Lowry using bovine serum albumin as a standard protein.

EXAMPLE 14

Production of recombinant OCIF using CHO cells

i) Construction of the plasmid for expressing OCIF

pBKOCIF containing about 1.6 kb OCIF cDNA was prepared as described in EXAMPLE 11, and digested with restriction enzymes, Sall and EcoRV. About 1.4 kb OCIF cDNA insert was separated by an agarose gel electrophoresis, and purified from the gel using QIAEX gel extraction kit (QIAGEN). The expression vector, pcDL-SR α 296 (Molecular and Cellular Biology, vol 8, p466, 1988) was digested with restriction enzymes, PstI and KpnI. About 3.4 kb of the expression vector fragment was cut out, separated by agarose gel electrophoresis, and purified from the gel using QIAEX gel extraction kit (QIAGEN). The ends of the purified OCIF cDNA insert and the expression vector fragment were blunted using DNA blunting kit (Takara Shuzo). The purified OCIF cDNA insert and the expression vector fragment were ligated using DNA ligation kit ver. 2 (Takara Shuzo). E.coli. DH5a α (Gibco BRL) was transformed with the ligation mixture. The transformant containing the OCIF expression plasmid, pSR α OCIF was obtained.

ii) Preparation of expression plasmid

The transformant containing the OCIF expression plasmid, pSR α OCIF prepared in the example 13-i) and the transformant containing the mouse DHFR expression plasmid, pBAdDSV shown in WO92/01053 were grown according to the standard method. Both plasmids were purified by alkali treatment, polyethylene glycol precipitation, and cesium chrolide density gradient ultra centrifugation according to method of Maniatis et al. (Molecular cloning, 2nd edition).

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iii) Adaptation of CHOdhFr- cells to the protein free medium

CHOdhFr- cells (ATCC, CRL 9096) were cultured in IMDM containing 10 % fetal calf serum. The cells were adapted to EX-CELL 301 (JRH Bioscience) and then adapted to EX-CELL PF CHO (JRH Bioscience) according to the manufacturer's instructions.

iv) Transfection of the OCIF expression plasmid, and the mouse DHFR expression plasmid, to CHOdhFr- cells.

CHOdhFr- cells prepared in EXAMPLE 14-iii) were transfected by electroporation with pSR α OCIF and pBAdDSV prepared in EXAMPLE 14-ii). 200 μ g of pSR α OCIF and 20 μ g of pBAdDSV were dissolved under sterile conditions in 0.8 ml of IMDM (Gibco BRL) containing 10 % fetal calf serum. 2×10^7 cells of CHOdhFr- were suspended in 0.8 ml of this medium. The cell suspension was transferred to a cuvette (Bio Rad) and the cells were transfected by electroporation using gene pulser (Bio Rad) under condition of 360 V and 960 μ F. The suspension of electroporated cells was transferred to T-flasks (Sumitomo Bakelite) containing 10 ml of EX-CELL PF-CHO, and incubated in the CO₂ incubator for 2 days. Then the transfected cells were inoculated in each well of a 96 well plate (Sumitomo Bakelite) at a density of 5000 cells/well and cultured for about 2 weeks. The transformants expressing DHFR are selected since EX-CELL PF-CHO does not contain nucleotides and the parental cell line CHO dhFr- can not grow in this medium. Most of the transformants expressing DHFR express OCIF since the OCIF expression plasmid was used ten times as much as the mouse DHFR expression plasmid. The transformants whose conditioned medium had high OCIF activity were selected among the transformants expressing DHFR according to the method described in EXAMPLE 2. The transformants that express large amounts of OCIF were cloned by limiting dilution. The clones whose conditioned medium had high OCIF activity were selected as described above and the transformant expressing large amount of OCIF, 5561, was obtained.

v) Production of recombinant OCIF

To produce recombinant OCIF (rOCIF), EX-CELL 301 medium (3 l) in a 3 l-spiner flask was inoculated with the clone (5561) at a cell-density of 1×10^5 cells/ml. The 5561 cells were cultured in a spiner flask at 37°C for 4 to 5 days. When the concentration of the 5561 cells reached to 1×10^6 cells/ml, about 2.7 l of the conditioned medium was harvested. Then about 2.7 l of EX-CELL 301 was added to the spiner flask and the 5561 cells were cultured repeatedly. About 20 l of the conditioned medium was harvested using the three spiner flasks.

vi) Isolation of recombinant OCIF protein from CHO cells-conditioned medium

CHO cells-conditioned medium (1.0 l) described in EXAMPL 14-v) was supplemented with 1.0 g of CHAPS and filtered with 0.22 μ m membrane filter (Steribecks GS, Milipore Co.). The conditioned medium was applied to a heparin Sepharose-FF column (2.6 x 10 cm, Pharmacia Co.) equilibrated with 10 mM Tris-HCl, pH 7.5. After washing the column with 10 mM Tris-HCl, 0.1 % CHAPS, pH 7.5, the adsorbed protein was eluted from the column with linear gradient from 0 to 2 M NaCl at a flow rate of 4 ml/min for 100 min. and fractions (8 ml) were collected. Using 150 μ l of each fraction, OCIF activity was assayed according to the method described in EXAMPLE 2. Active fraction (112 ml) eluted with approximately 0.6 to 1.2 M NaCl was obtained.

The 112 ml of active fraction was diluted to 1200 ml with 10 mM Tris-HCl, 0.1% CHAPS, pH 7.5, and applied to a affinity column (blue-5PW, 0.5 x 5.0 cm, Tosoh Co.) equilibrated with 10 mM Tris-HCl, 0.1% CHAPS, pH 7.5. After washing the column with 10 mM Tris-HCl, 0.1% CHAPS, pH 7.5, the adsorbed protein was eluted from the column with linear gradient from 0 to 3 M NaCl at a flow rate of 0.5ml/min for 60 min., and fractions (0.5 ml) were collected. Four μ l of each fraction was subjected to SDS-polyacrylamide gel electrophoresis under reducing and non-reducing conditions as described in EXAMPLE 4. On SDS-PAGE under reducing conditions, a single band of rOCIF protein with apparent 60 KD was detected in fractions 30 to 38, under non-reducing conditions, bands of rOCIF protein with apparent 60 KD and 120 KD were also detected in fractions 30 to 38. The isolated rOCIF fraction, 30 to 38, was designated as purified recombinant OCIF derived from CHO cells (rOCIF(C)). 4.5 ml of the rOCIF(C) (113 μ g/ml) was obtained when determined by the method of Lowry using bovine serum albumin as a standard protein.

EXAMPLE 15

Determination of N-terminal amino acid sequence of rOCIFs

Each 3 μ g of the isolated rOCIF(E) and rOCIF(C) was adsorbed to polyvinylidene difluoride (PVDF) membranes with Prosipin (PERKIN ELMER Co.). The membranes were washed with 20 % ethanol and the N-terminal amino acid sequences of the adsorbed proteins were analyzed by protein sequencer (PROCISE 492, PERKIN ELMER Co.). The

determined N-terminal amino acid sequence is shown in sequence No. 7.

The N-terminal amino acid of rOCIF(E) and rOCIF(C) was the 22th amino acid of glutamine from Met as translation starting point, as shown in sequence number 5. The 21 amino acids from Met to Gln were identified as a signal peptide. The N-terminal amino acid sequence of OCIF isolated from IMR-90 conditioned medium was undetectable. Accordingly, the N-terminal glutamine of OCIF may be blocked by converting from glutamine to pyroglutamine within culturing or purifying.

EXAMPLE 16

10 Biological activity of recombinant(r) OCIF and natural(n) OCIF

i) Inhibition of vitamin D₃ induced osteoclast formation from murine bone marrow cells

Each the rOCIF(E) and nOCIF sample was diluted with α -MEM (GIBCO BRL Co.) containing 10% FBS and 2×10^{-8} M of activated vitamin D₃ (a final concentration of 250 ng/ml). Each sample was serially diluted with the same medium, and 100 μ l of each diluted sample was added to each well in 96-well plates. Bone marrow cells obtained from mice, 17 days-old, were inoculated at a cell density of 3×10^5 cells/100 μ l/well to each well in 96-well plates and cultured for 7 days at 37°C in humidified 5%CO₂. On day 7, the cells were fixed and stained with a acid phosphatase measuring kit (Acid Phosphatase, Leucocyte, No387-A, Sigma) according to the method described in EXAMPLE 2. The decrease of acid phosphatase activity (TRAP) was taken as OCIF activity. The decrease of acid phosphatase-positive cells was evaluated by solubilizing the pigment of dye and measuring absorbance. In detail, 100 μ l of a mixture of 0.1 N NaOH and dimethylsulfoxide (1:1) was added to each well and the well was vibrated to solubilize the dye. After solubilizing the dye completely, an absorbance of each well was measured at 590 nm subtracting the absorbance at 490 nm using microplate reader (Immunoreader NJ-2000, InterMed). The microplate reader was adjusted to 0 absorbance using a well with monolayered bone marrow cells which was cultured in the medium without activated vitamin D₃. The decrease of TRAP activity was expressed as a percentage of the control absorbance value (=100%) of the solubilized dye from wells with bone marrow cells which were cultured in the absence of OCIF. The results are shown in Table 5.

Table 5

Inhibition of vitamin D ₃ -induced osteoclast formation from murine bone marrow cells						
OCIF concentration(ng/ml)	250	125	63	31	16	0
rOCIF(E)	0	0	3	62	80	100
nOCIF	0	0	27	27	75	100 (%)

Both nOCIF and rOCIF(E) inhibited osteoclast formation in a dose dependent manner in the concentration of 16 ng/ml or higher

ii) Inhibition of vitamin D₃-induced osteoclast formation in co-cultures of stromal cells and mouse spleen cells.

Effect of OCIF on osteoclast formation induced by Vitamin D₃ in co-cultures of stromal cells and mouse spleen cells was tested according to the method of N. Udagawa et al. (Endocrinology, vol. 125, p1805-1813, 1989). In detail, each of rOCIF(E), rOCIF(C), and nOCIF sample was serially diluted with α -MEM (GIBCO BRL Co.) containing 10% FBS, 2×10^{-8} M of activated vitamin D₃, and 2×10^{-7} M dexamethasone, and 100 μ l of each the diluted samples was added to each well in 96 well-microwell plates. Murine bone marrow-derived stromal ST2 cells (RIKEN Cell Bank RCB0224) ; 5×10^3 cells per 100 μ l of α -MEM containing 10% FBS, and spleen cells from ddy mice, 8 weeks-old, ; 1×10^5 cells per 100 μ l in the same medium, were inoculated to each well in 96-well plates and cultured for 5 days at 37°C in humidified 5%CO₂. On day 5, the cells were fixed and stained with a kit for acid phosphatase (Acid Phosphatase, Leucocyte, No387-A, Sigma). The decrease of acid phosphatase-positive cells was taken as OCIF activity. The decrease of acid phosphatase-positive cells was evaluated according to the method described in EXAMPLE 16-i). The results are shown in Table 6 ; rOCIF(E) and rOCIF(C), and Table 7 ; rOCIF(E) and nOCIF.

Table 6

Inhibition of osteoclast formation in co-cultures of stromal cells and mouse spleen cells.					
OCIF concentration(ng/ml)	50	25	13	6	0
rOCIF(E)	3	22	83	80	100
rOCIF(C)	13	19	70	96	100 (%)

Table 7

Inhibition of osteoclast formation in co-cultures of stromal cells and mouse spleen cells.				
OCIF concentration(ng/ml)	250	63	16	0
rOCIF(E)	7	27	37	100
rOCIF(C)	13	23	40	100 (%)
nOCIF, rOCIF(E) and rOCIF(C) inhibited osteoclast formation in a dose dependent manner in the concentration of 6 - 16 ng/ml or higher				

iii) Inhibition of PTH-induced osteoclast formation from murine bone marrow cells.

Effect of OCIF on osteoclast formation induced by PTH was tested according to the method of N. Takahashi et al. (Endocrinology, vol. 122, p1373-1382, 1988). In detail, each the rOCIF(E) and nOCIF sample (125 ng/ml) was serially diluted with α -MEM (manufactured by GIBCO BRL Co.) containing 10% FBS and 2×10^{-8} M PTH, and 100 μ l of each the diluted samples was added to 96 well-plates. Bone marrow cells from ddy mice, 17 days-old, at a cell density of 3×10^5 cells per 100 μ l of α -MEM containing 10% FBS were inoculated to each well in 96-wells plates and cultured for 5 days at 37°C in humidified 5%CO₂. On day 5, the cells were fixed with ethanol/acetone (1:1) for 1 min. at room temperature and stained with a kit for acid phosphatase (Acid Phosphatase, Leucocyte, No387-A, Sigma) according to the method described in EXAMPLE 2. The decrease of acid phosphatase-positive cells was taken as OCIF activity. The decrease of acid phosphatase-positive cells was evaluated according to the method described in EXAMPLE 16-i). The results are shown in Table 8.

Table 8

Inhibition of PTH-induced osteoclast formation from murine bone marrow cells.						
OCIF concentration(ng/ml)	125	63	31	16	8	0
rOCIF(E)	6	58	58	53	88	100
nOCIF	18	47	53	56	91	100
nOCIF and rOCIF(E) inhibited osteoclast formation in a dose dependent manner in the concentration of 16 ng/ml or higher						

iv) Inhibition of IL-11-induced osteoclast formation

Effect of OCIF on osteoclast formation induced by IL-11 was tested according to the method of T. Tamura et al. (Proc. Natl. Acad. Sci. USA, vol. 90, p11924-11928, 1993). In detail, each rOCIF(E) and nOCIF sample was serially

diluted with α -MEM (GIBCO BRL Co.) containing 10% FBS and 20 ng/ml IL-11 and 100 μ l of each the diluted sample was added to each well in 96-well plates. Newborn mouse calvaria-derived pre-adipocyte MC3T3-G2/PA6 cells (RIKEN Cell Bank RCB1127) ; 5×10^3 cells per 100 μ l of α -MEM containing 10% FBS, and spleen cells from ddy mouse, 8 weeks-old, ; 1×10^5 cells per 100 μ l in the same medium, were inoculated to each well in 96-well plates and cultured for 5 days at 37 °C in humidified 5%CO₂. On day 5, the cells were fixed and stained with a kit for acid phosphatase (Acid Phosphatase, Leucocyte, No387-A, Sigma). Acid phosphatase positive cells were counted under microscope and a decrease of the cell numbers was taken as OCIF activity. The results are shown in Table 9.

Table 9

OCIF concentration(ng/ml)	500	125	31	7.8	2.0	0.5	0
nOCIF	0	0	1	4	13	49	31
rOCIF(E)	0	0	1	3	10	37	31
Both nOCIF and rOCIF(E) inhibited osteoclast formation in a dose dependent manner in the concentration of 2 ng/ml or higher							

The results shown in Table 4-8 indicated that OCIF inhibits all the vitamin D₃, PTH, and IL-11-induced osteoclast formations at almost the same doses. Accordingly, OCIF would be able to be used for treatment of the different types of bone disorders with decreased bone mass, which are caused by different substances which induce bone resorption.

EXAMPLE 17

Isolation of monomer-type OCIF and dimer-type OCIF

Each rOCIF(E) and rOCIF(C) sample containing 100 μ g of OCIF protein, was supplemented with 1/100 volume of 25 % trifluoro acetic acid and applied to a reverse phase column (PROTEIN-RP, 2.0x250 mm, YMC Co.) equilibrated with 30 % acetonitrile containing 0.1 % trifluoro acetic acid. OCIF protein was eluted from the column with linear gradient from 30 to 55 % acetonitrile at a flow rate of 0.2 ml/min for 50 min. and each OCIF peak was collected. Each the monomer-type OCIF peak fraction and dimer-type OCIF peak fraction was lyophilized, respectively.

EXAMPLE 18

Determination of molecular weight of recombinant OCIFs

Each 1 μ g of the isolated monomer-type and dimer-type nOCIF purified using reverse phase column according to EXAMPLE 3-iv) and each 1 μ g of monomer-type and dimer-type rOCIF described in EXAMPLE 17 was concentrated under vacuum, respectively. Each sample was incubated in the buffer for SDS-PAGE, subjected to SDS-polyacrylamide gel electrophoresis, and protein bands on the gel were stained with silver according to the method described in EXAMPLE 4. Results of electrophoresis under non-reducing conditions and reducing conditions are shown in Figure 6 and Figure 7.

A protein band with an apparent molecular weight of 60 KD was detected in each monomer-type OCIF sample, and a protein band with an apparent molecular weight of 120 KD was detected in each dimer-type OCIF sample in non-reducing conditions. A protein band with an apparent molecular weight of 60 KD was detected in each monomer-type OCIF sample under reducing conditions. Accordingly, molecular weights of monomer-type nOCIF from IMR-90 cells, rOCIF from 293/EBNA cells and rOCIF from CHO cells were almost the same. Molecular weights of dimer-type nOCIF from IMR-90 cells, rOCIF from 293/EBNA cells, and rOCIF from CHO cells were also the same.

EXAMPLE 19

Remove N-linked Oligosaccharide chain and Mesuring molecular weight of natural and recombinant OCIF

Each sample containing 5 μ g of the isolated monomer-type and dimer-type nOCIF purified using reverse phase column according to EXAMPLE 3-iv) and each sample containing 5 μ g of monomer-type and dimer-type rOCIF described in EXAMPLE 17 were concentrated under vacuum. Each sample was dissolved in 9.5 μ l of 50 mM sodium phosphate buffer, pH 8.6, containing 100 mM 2-mercaptoethanol, supplemented with 0.5 μ l of 250 U/ml N-glycanase (Seikagaku

kogyo Co.) and incubated for one day at 37 °C. Each sample was supplemented with 10 µl of 20 mM Tris-HCl, pH 8.0 containing 2 mM EDTA, 5 % SDS, and 0.02 % bromo-phenol blue and heated for 5 min at 100 °C. Each 1 µl of the samples was subjected to SDS-polyacrylamide gel electrophoresis, and protein bands on the gel were stained with silver as described in EXAMPLE 4. The patterns of electrophoresis are shown in Figure 8.

5 An apparent molecular weight of each the deglycosylated nOCIF from IMR-90 cells, rOCIF from CHO cells, and rOCIF from 293/EBNA cells was 40 KD under reducing conditions. An apparent molecular weight of each untreated nOCIF from IMR-90 cells, rOCIF from 293/EBNA cells, and rOCIF from CHO cells was 60 KD under reducing conditions. Accordingly, the results indicate that the OCIF proteins are glycoproteins with N-linked sugar chains.

10 EXAMPLE 20

Cloning of OCIF variant cDNAs and determination of their DNA sequences

The plasmid pBKOCIF, which is inserted OCIF cDNA to pBKCMV (Stratagene), was obtained from one of some purified positive phage as in example 10 and 11. And more, during the screening of the cDNA library with the 397 bp OCIF cDNA probe, the transformants containing plasmids whose insert sizes were different from that of pBKOCIF were obtained. These transformants containing the plasmids were grown and the plasmids were purified according to the standard method. The sequence of the insert DNA in each plasmid was determined using Taq Dye Deoxy Terminator Cycle Sequencing kit (Perkin Elmer). The used primers were T3, T7 primers (Stratagene) and synthetic primers prepared based on the nucleotide sequence of OCIF cDNA. There are four OCIF variants (OCIF2, 3, 4, and 5) in addition to OCIF. The nucleotide sequence of OCIF2 is shown in the sequence number 8 and the amino acid sequence of OCIF 2 predicted by the nucleotide sequence is shown in the sequence number 9. The nucleotide sequence of OCIF3 is shown in the sequence number 10 and the amino acid sequence of OCIF3 predicted by the nucleotide sequence is shown in the sequence number 11. The nucleotide sequence of OCIF4 is shown in the sequence number 12 and the amino acid sequence of OCIF4 predicted by the nucleotide sequence is shown in the sequence number 13. The nucleotide sequence of OCIF5 is shown in the sequence number 14 and the amino acid sequence of OCIF5 predicted by the nucleotide sequence is shown in the sequence number 15. The structures of OCIF variants are shown in Figures 9 to 12 and are described in brief below. OCIF2

30 OCIF2 cDNA has a deletion of 21 bp from guanine at nucleotide number 265 to guanine at nucleotide number 285 in OCIF cDNA (sequence number 6). Accordingly OCIF2 has a deletion of 7 amino acids from glutamic acid (Glu) at amino acid number 68 to glutamine (Gln) at amino acid number 74 in OCIF (sequence number 5).

OCIF3

35 OCIF3 cDNA has a point mutation at nucleotide number 9 in OCIF cDNA (sequence number 6) where cytidine is replaced with guanine.

Accordingly OCIF3 has a mutation and asparagine (Asn) at amino acid number -19 in OCIF (sequence number 5) is replaced with lysine (Lys). The mutation seems to be located in the signal sequence and have no essential effect on the secreted OCIF3. OCIF3 cDNA has a deletion of 117 bp from guanine at nucleotide number 872 to cytidine at nucleotide number 988 in OCIF cDNA (sequence number 6).

40 Accordingly OCIF3 has a deletion of 39 amino acids from threonine (Thr) at amino acid number 270 to leucine (Leu) at amino acid number 308 in OCIF (sequence number 5).

OCIF4

45 OCIF4 cDNA has two point mutations in OCIF cDNA (sequence number 6). Cytidine at nucleotide number 9 is replaced with guanine and guanine at nucleotide number 22 is replaced with thymidine in OCIF cDNA (sequence number 6).

50 Accordingly OCIF4 has two mutations. Asparagine (Asn) at amino acid number -19 in OCIF (sequence number 5) is replaced with lysine (Lys), and alanine (Ala) at amino acid number -14 is replaced with serine (Ser). These mutations seem to be located in the signal sequence and have no essential effect on the secreted OCIF4.

OCIF4 cDNA has about 4 kb DNA, which is the intron 2 of OCIF gene, inserted between nucleotide number 400 and nucleotide number 401 in OCIF cDNA (sequence number 6). The open reading frame stops in intron 2.

55 Accordingly OCIF4 has an additional novel amino acid sequence containing 21 amino acids after alanine (Ala) at amino acid number 112 in OCIF (sequence number 5).

OCIF5

OCIF5 cDNA has a point mutation at nucleotide number 9 in OCIF cDNA (sequence number 6) where cytidine is replaced with guanine.

- 5 Accordingly OCIF5 has a mutation and asparagine (Asn) at amino acid number -19 in OCIF (sequence number 5) is replaced with lysine (Lys). The mutation seems to be located in the signal sequence and have no essential effect on the secreted OCIF5.

OCIF5 cDNA has the latter portion (about 1.8 kb) of intron 2 between nucleotide number 400 and nucleotide number 401 in OCIF cDNA (sequence number 6). The open reading frame stops in the latter portion of intron 2.

- 10 Accordingly OCIF5 has an additional novel amino acid sequence containing 12 amino acids after alanine (Ala) at amino acid number 112 in OCIF (sequence number 5).

EXAMPLE 21

15 Production of OCIF variants

i) Construction of the plasmid for expressing OCIF variants

The plasmid containing OCIF2 or OCIF3 cDNA was obtained as described in EXAMPLE 20 and called pBKOCIF2 and pBKOCIF3, respectively. pBKOCIF2 and pBKOCIF3 were digested with restriction enzymes, BamHI and XhoI. The OCIF2 and OCIF3 cDNA inserts were separated by agarose gel electrophoresis, and purified from the gel using QIAEX gel extraction kit (QIAGEN). The purified OCIF2 and OCIF3 cDNA inserts were individually ligated using DNA ligation kit ver. 2 (Takara Shuzo) to the expression vector pCEP4 (Invitrogen) that had been digested with restriction enzymes, BamHI and XhoI. E. coli. DH5 α (Gibco BRL) was transformed with the ligation mixture.

25 The plasmid containing OCIF4 cDNA was obtained as described in EXAMPLE 20 and called pBKOCIF4. pBKOCIF4 was digested with restriction enzymes, SpeI and XhoI (Takara Shuzo). The OCIF4 cDNA insert was separated by an agarose gel electrophoresis, and purified from the gel using QIAEX gel extraction kit (QIAGEN). The purified OCIF4 cDNA insert was ligated using DNA ligation kit ver. 2 (Takara Shuzo) to the expression vector pCEP4 (Invitrogen) that had been digested with restriction enzymes, NheI and XhoI (Takara Shuzo). E.coli. DH5 α (Gibco BRL) was transformed with the ligation mixture.

30 The plasmid containing OCIF5 cDNA was obtained as described in EXAMPLE 20 and was called pBKOCIF5. pBKOCIF5 was digested with restriction enzyme, HindIII (Takara Shuzo). The 5' portion of the coding region in the OCIF5 cDNA insert was separated by agarose gel electrophoresis, and purified from the gel using QIAEX gel extraction kit (QIAGEN). The OCIF expression plasmid, pCEPOCIF, obtained in EXAMPLE 13-i) was digested with restriction enzyme, HindIII (Takara Shuzo). The 5' portion of the coding region in the OCIF cDNA was removed. The rest of the plasmid that contains pCEP vector and the 3' portion of the coding region of OCIF cDNA was called pCEPOCIF-3'. pCEPOCIF-3' was separated by an agarose gel electrophoresis, and purified from the gel using QIAEX gel extraction kit (QIAGEN). The OCIF5 cDNA HindIII fragment and pCEPOCIF-3' were ligated using DNA ligation kit ver. 2 (Takara Shuzo). E.coli. DH5 α (Gibco BRL) was transformed with the ligation mixture.

40 The obtained transformants were grown at 37 °C overnight and the OCIF variants expression plasmids (pCEPOCIF2, pCEPOCIF3, pCEPOCIF4, and pCEPOCIF5) were purified using QIAGEN column (QIAGEN). These OCIF-variants-expression plasmids were precipitated with ethanol, dissolved in sterile distilled water, and used in the experiments described below.

45 ii) Transient expression of OCIF variant cDNAs and analysis of the biological activity of recombinant OCIF variants.

Recombinant OCIF variants were produced using the expression plasmid, pCEPOCIF2, pCEPOCIF3, pCEPOCIF4, and pCEPOCIF5 prepared as described in EXAMPLE 21-i) according to the method described in EXAMPLE 13-ii). The biological activities of recombinant OCIF variants were analyzed. The results were that these OCIF variants (OCIF2, OCIF3, OCIF4, and OCIF5) had a weak activity.

EXAMPLE 22

Preparation of OCIF mutants

55

i) Construction of a plasmid vector for subcloning cDNAs encoding OCIF mutants

The plasmid vector (5 μ g) described in EXAMPLE 11 was digested with restriction enzymes Bam HI and Xho I (

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Takara Shuzo). The digested DNA was subjected to a preparative agarose gel electrophoresis. DNA fragment with an approximate size of 1.6 kilobase pairs (kb) that contained the entire coding sequence for OCIF was purified from the gel using QIAEX gel extraction kit (QIAGEN). The purified DNA was dissolved in 20 μ l of sterile distilled water. This solution was designated DNA solution 1. p Bluescript II SK + (3 μ g) (Stratagene) was digested with restriction enzymes Bam HI and Xho I (Takara Shuzo). The digested DNA was subjected to preparative agarose gel electrophoresis. DNA fragment with an approximate size of 3.0 kb was purified from the gel using QIAEX DNA extraction kit (QIAGEN). The purified DNA was dissolved in 20 μ l of sterile distilled water. The solution was designated DNA solution 2. One microliter of DNA solution 2, 4 μ l of DNA solution 1 and 5 μ l of ligation buffer I of DNA ligation kit ver. 2 (Takara Shuzo) were mixed and incubated at 16 °C for 30 min. (The ligation mixture was used for the transformation of E. coli in a manner described below). Conditions for transformation of E. coli were as follows. One hundred microliters of competent E. coli DH5 α cells (GIBCO BRL) and 5 μ l of the ligation mixture was mixed in a sterile 15-ml tube (IWAKI glass). The tube was kept on ice for 30 min. After incubation for 45 sec at 42°C, to the cells was added 250 μ l of L broth (1% Tryptone, 0.5% yeast extract, 1% NaCl). The cell suspension was then incubated for 1 hr. at 37°C with shaking. Fifty microliters of the cell suspension was plated onto an L-agar plate containing 50 μ g/ml of ampicillin. The plate was incubated overnight at 37°C.

Six colonies which grew on the plate were individually incubated in 2 ml each of L-broth containing 50 μ g/ml of ampicillin overnight at 37°C with shaking. The structure of the plasmids in the colonies was analyzed. A plasmid in which the 1.6-kb DNA fragment containing the entire OCIF cDNA is inserted between the digestion sites of Bam HI and Xho I of pBluescript II SK + was obtained and designated as pSK + -OCIF.

ii) Preparation of mutants in which one of the Cys residues in OCIF is replaced with Ser residue

1) Introduction of mutations into OCIF cDNA

OCIF mutants were prepared in which one of the five Cys residues present in OCIF at positions 174, 181, 256, 298 and 379 (in SEQUENCE NO 4) was replaced with Ser residue and were designated OCIF-C19S(174Cys to Ser), OCIF-C20S (181Cys to Ser), OCIF-C21S (256Cys to Ser), OCIF-C22S (298Cys to Ser) and OCIF-C23S (379Cys to Ser), respectively.

To prepare the mutants, nucleotides encoding the corresponding Cys residues were replaced with those encoding Ser. Mutagenesis was carried out by a two-step polymerase chain reaction (PCR). The first step of the PCRs consisted of two reactions, PCR 1 and PCR 2.

PCR 1	10X Ex Taq Buffer (Takara Shuzo)	10 μ l
	2.5 mM solution of dNTPs	8 μ l
	the plasmid vector described in EXAMPLE 11 (8ng/ml)	2 μ l
	sterile distilled water	73.5 μ l
	20 μ M solution of primer 1	5 μ l
	100 μ M solution of primer 2 (for mutagenesis)	1 μ l
PCR 2	Ex Taq (Takara Shuzo)	0.5 μ l
	10X Ex Taq Buffer (Takara Shuzo)	10 μ l
	2.5 mM solution of dNTPs	8 μ l
	the plasmid vector described in EXAMPLE 11 (8ng/ml)	2 μ l
	sterile distilled water	73.5 μ l
	20 μ M solution of primer 3	5 μ l
	100 μ M solution of primer 4 (for mutagenesis)	1 μ l
	Ex Taq (Takara Shuzo)	0.5 μ l

Specific sets of primers were used for each mutation and other components were unchanged. Primers used for the reactions are shown in Table 10. The nucleotide sequences of the primers are shown in SEQUENCE NO: 20,23,27 and 30-40. The PCRs were performed under the following conditions as follows. An initial denaturation step at 97°C for 3 min was followed by 25 cycles of denaturation at 95°C for 1 min annealing at 55°C for 1 min and extension at 72°C for

3 min. After these amplification cycles, final extension was performed at 70°C for 5 min. The size of the PCR products was confirmed by agarose gel electrophoresis using reaction solution. After the first PCR, excess primers were removed using Amicon microcon (Amicon). The final volume of the solutions that contained the PCR products were made to 50 µl with sterile distilled water. These purified PCR products were used for the second PCR (PCR 3).

PCR 3	10X Ex Taq Buffer (Takara Shuzo)	10 µl
	2.5 mM solution of dNTPs	8 µl
	solution containing DNA fragment obtained from PCR 1	5 µl
	solution containing DNA fragment obtained from PCR 2	5 µl
	sterile distilled water	61.5 µl
	20 µM solution of primer 1	5 µl
	20 µM solution of primer 3	5 µl
	Ex Taq (Takara Shuzo)	0.5 µl

Table 10

mutants	primer-1	primer-2	primer-3	primer-4
OCIF-C19S	IF 10	C19SR	IF 3	C19SF
OCIF-C20S	IF 10	C20SR	IF 3	C20SF
OCIF-C21S	IF 10	C21SR	IF 3	C21SF
OCIF-C22S	IF 10	C22SR	IF 14	C22SF
OCIF-C23S	IF 6	C23SR	IF 14	C23SF

The reaction conditions were exactly the same as those for PCR 1 or PCR 2. The size of the PCR products was confirmed by 1.0 % or 1.5 % agarose gel electrophoresis. The DNA fragments were precipitated with ethanol, dried under vacuum and dissolved in 40 µl of sterile distilled water. The solutions containing DNA fragments with mutation C19S, C20S, C21S, C22S and C23S were designated as DNA solution A, DNA solution B, DNA solution C, DNA solution D and DNA solution E, respectively.

The DNA fragment which is contained in solution A (20 µl) was digested with restriction enzymes Nde I and Sph I (Takara Shuzo). A DNA fragment with an approximate size of 400 base pairs (bp) was extracted from a preparative agarose gel and dissolved in 20 µl of sterile distilled water. This DNA solution was designated DNA solution 3. Two micrograms of pSK + -OCIF was digested with restriction enzymes Nde I and Sph I. A DNA fragment with an approximate size of 4.2 kb was purified from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 µl of sterile distilled water. This DNA solution was designated as DNA solution 4. Two microliters of DNA solution 3, 3 µl of DNA solution 4 and 5 µl of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent E. coli DH5 α cells were transformed with 5 µl of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-C19S.

The DNA fragment which is contained in solution B (20 µl) was digested with restriction enzymes Nde I and Sph I. A DNA fragment with an approximate size of 400 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 µl of sterile distilled water. This DNA solution was designated DNA solution 5. Two microliters of DNA solution 5, 3 µl of DNA solution 4 and 5 µl of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent E. coli DH5 α cells were transformed with 5 µl of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-C20S.

The DNA fragment which is contained in solution C (20 µl) was digested with restriction enzymes Nde I and Sph I. A DNA fragment with an approximate size of 400 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 µl of sterile distilled water. This DNA solution was designated as DNA solution 6. Two micro-

liters of DNA solution 6, 3 μ l of DNA solution 4 and 5 μ l of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent *E. coli* DH5 α cells were transformed with 5 μ l of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-C21S.

5 The DNA fragment which is contained in solution D (20 μ l) was digested with restriction enzymes Nde I and Bst PI. A DNA fragment with an approximate size of 600 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 μ l of sterile distilled water. This DNA solution was designated as DNA solution 7. Two micrograms of pSK + -OCIF was digested with restriction enzymes Nde I and Bst PI. A DNA fragment with an approximate size of 4.0 kb was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 μ l of sterile distilled water. This DNA solution was designated as DNA solution 8. Two microliters of DNA solution 7, 3 μ l of DNA solution 8 and 5 μ l of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent *E. coli* DH5 α cells were transformed with 5 μ l of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA in which the 600-bp Nde I-BstPI fragment with the mutation (the C22S mutation) is substituted for the 600-bp Nde I-Bst PI fragment of pSK+ -OCIF by analyzing the DNA structure. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-C22S.

The DNA fragment which is contained in solution E (20 μ l) was digested with restriction enzymes Bst PI and Eco RV. A DNA fragment with an approximate size of 120 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 μ l of sterile distilled water. This DNA solution was designated as DNA solution 9. Two micrograms of pSK + -OCIF was digested with restriction enzymes Bst EII and Eco RV. A DNA fragment with an approximate size of 4.5 kb was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 μ l of sterile distilled water. This DNA solution was designated as DNA solution 10. Two microliters of DNA solution 9, 3 μ l of DNA solution 10 and 5 μ l of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation was carried out. Competent *E. coli* DH5 α cells were transformed with 5 μ l of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-C23S.

2) Construction of vectors for expressing the OCIF mutants

30 pSK-OCIF-C19S, pSK-OCIF-C20S, pSK-OCIF-C21S, pSK-OCIF-C22S and pSK-OCIF-C23S were digested with restriction enzymes Bam HI and Xho I. The 1.6 kb Bam HI-Xho I DNA fragment encoding each OCIF mutant was isolated and dissolved in 20 μ l of sterile distilled water. The DNA solutions that contain 1.6 kb cDNA fragments derived from pSK-OCIF-C19S, pSK-OCIF-C20S, pSK-OCIF-C21S, pSK-OCIF-C22S and pSK-OCIF-C23S were designated C19S DNA solution, C20S DNA solution, C21S DNA solution, C22S DNA solution and C23S DNA solution, respectively. Five micrograms of a expression vector pCEP 4 (Invitrogen) was digested with restriction enzymes Bam HI and Xho I. A DNA fragment with an approximate size of 10 kb was purified and dissolved in 40 μ l of sterile distilled water. This DNA solution was designated as pCEP 4 DNA solution. One microliter of pCEP 4 DNA solution and 6 μ l of either C19SDNA solution, C20S DNA solution, C21S DNA solution, C22S DNA solution or C23S DNA solution were independently mixed with 7 μ l of ligation buffer I of DNA ligation kit ver. 2 and ligation reactions were carried out. Competent *E. coli* DH5 α cells (100 μ l) were transformed with 7 μ l of each ligation mixture. Ampicillin-resistant transformants were screened for clones containing plasmid in which a 1.6-kb cDNA fragment is inserted between the recognition sites of Bam HI and Xho I of pCEP 4 by analyzing the DNA structure. The plasmids which were obtained containing the cDNA encoding OCIF-C19S, OCIF-C20S, OCIF-C21S, OCIF-C22S and OCIF-C23S were designated pCEP4-OCIF-C19S, pCEP4-OCIF-C20S, pCEP4-OCIF-C21S, pCEP4-OCIF-C22S and pCEP4-OCIF-C23S, respectively.

ii) Preparation of domain-deletion mutants of OCIF

(1) deletion mutagenesis of OCIF cDNA

50 A series of OCIF mutants with deletions of from Thr 2 to Ala 42, from Pro 43 to Cys 84, from Glu 85 to Lys 122, from Arg 123 to Cys 164, from Asp 177 to Gln 251 and from Ile 252 to His 326 were prepared (positions of the amino acid residues are shown in SEQUENCE NO: 4). These mutants were designated as OCIF-DCR1, OCIF-DCR2, OCIF-DCR3, OCIF-DCR4, OCIF-DDD1 and OCIF-DDD2, respectively.

Mutagenesis was performed by two-step PCR as described in EXAMPLE 22-(ii). The primer sets for the reactions are shown in Table 11 and the nucleotide sequences of the primers are shown in SEQUENCE NO: 19, 25, 40-53, and 54.

Table 11

mutants	primer-1	primer-2	primer-3	primer-4
OCIF-DCR1	XhoI F	DCR1R	IF 2	DCR1F
OCIF-DCR2	XhoI F	DCR2R	IF 2	DCR2F
OCIF-DCR3	XhoI F	DCR3R	IF 2	DCR3F
OCIF-DCR4	XhoI F	DCR4R	IF 16	DCR4F
OCIF-DDD1	IF 8	DDD1R	IF 14	DDD1F
OCIF-DDD2	IF 8	DDD2R	IF 14	DDD2F

The final PCR products were precipitated with ethanol, dried under vacuum and dissolved in 40 µl of sterile distilled water. Solutions of DNA fragment coding for portions of OCIF-DCR1, OCIF-DCR2, OCIF-DCR3, OCIF-DCR4, OCIF-DDD1 and OCIF-DDD2 were designated as DNA solutions F, G, H, I, J and K, respectively.

The DNA fragment which is contained in solution F (20 µl) was digested with restriction enzymes Nde I and Xho I. A DNA fragment with an approximate size of 500 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 µl of sterile distilled water. This DNA solution was designated DNA solution 11. Two micrograms of pSK+ -OCIF was digested with restriction enzymes Nde I and Xho I. A DNA fragment with an approximate size of 4.0 kb was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 µl of sterile distilled water. This DNA solution was designated DNA solution 12. Two microliters of DNA solution 11, 3 µl of DNA solution 12 and 5 µl of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation was carried out. Competent *E. coli* DH5 α cells were transformed with 5 µl of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-DCR1.

The DNA fragment which is contained in solution G (20 µl) was digested with restriction enzymes Nde I and Xho I. A DNA fragment with an approximate size of 500 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 µl of sterile distilled water. This DNA solution was designated as DNA solution 13. Two microliters of DNA solution 13, 3 µl of DNA solution 12 and 5 µl of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation was carried out. Competent *E. coli* DH5α cells were transformed with 5 µl of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-DCR2.

The DNA fragment which is contained in solution H (20 µl) was digested with restriction enzymes Nde I and Xho I. A DNA fragment with an approximate size of 500 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 µl of sterile distilled water. This DNA solution was designated as DNA solution 14. Two microliters of DNA solution 14, 3 µl of DNA solution 12 and 5 µl of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent *E. coli* DH5 α cells were transformed with 5 µl of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-DCR3.

The DNA fragment which is contained in solution I (20 µl) was digested with restriction enzymes Xho I and Sph I. A DNA fragment with an approximate size of 900 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 µl of sterile distilled water. This DNA solution was designated as DNA solution 15. Two micrograms of pSK+ -OCIF was digested with restriction enzymes Xho I and Sph I. A DNA fragment with an approximate size of 3.6 kb was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 µl of sterile distilled water. This DNA solution was designated as DNA solution 16. Two microliters of DNA solution 15, 3 µl of DNA solution 16 and 5 µl of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent *E. coli* DH5 α cells were transformed with 5 µl of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-DCR4.

The DNA fragment which is contained in solution J (20 µl) was digested with restriction enzymes BstP I and Nde I. A DNA fragment with an approximate size of 400 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 µl of sterile distilled water. This DNA solution was designated as DNA solution 17. Two microliters of DNA solution 17, 3 µl of DNA solution 8 and 5 µl of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent *E. coli* DH5 α cells were transformed with 5 µl of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by

restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-DDD1. The DNA fragment which is contained in solution K (20 μ l) was digested with restriction enzymes Nde I and BstP I. A DNA fragment with an approximate size of 400 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 μ l of sterile distilled water. This DNA solution was designated as DNA solution 18. Two microliters of DNA solution 18, 3 μ l of DNA solution 8 and 5 μ l of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent *E. coli* DH5 α cells were transformed with 5 μ l of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-DDD2.

2) Construction of vectors for expressing the OCIF mutants

pSK-OCIF-DCR1, pSK-OCIF-DCR2, pSK-OCIF-DCR3, pSK-OCIF-DCR4, pSK-OCIF-DDD1 and pSK-OCIF-DDD2 were digested with restriction enzymes Bam HI and Xho I. The Bam HI-Xho I DNA fragment containing entire coding sequence for each OCIF mutant was isolated and dissolved in 20 μ l of sterile distilled water. These DNA solutions that contain the Bam HI-Xho I fragment derived from pSK-OCIF-DCR1, pSK-OCIF-DCR2, pSK-OCIF-DCR3, pSK-OCIF-DCR4, pSK-OCIF-DDD1 and pSK-OCIF-DDD2 were designated DCR1 DNA solution, DCR2 DNA solution, DCR3 DNA solution, DCR4 DNA solution, DDD1 DNA solution and DDD2 DNA solution, respectively. One microliter of pCEP 4 DNA solution and 6 μ l of either DCR1 DNA solution, DCR2 DNA solution, DCR3 DNA solution, DCR4 DNA solution, DDD1 DNA solution or DDD2 DNA solution were independently mixed with 7 μ l of ligation buffer I of DNA ligation kit ver. 2 and ligation reactions were carried out. Competent *E. coli* DH5 α cells (100 μ l) were transformed with 7 μ l of each ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA in which the DNA fragment with deletions is inserted between the recognition sites of Bam HI and Xho I of pCEP 4 by analyzing the DNA structure. The plasmids containing the cDNA encoding OCIF-DCR1, OCIF-DCR2, OCIF-DCR3, OCIF-DCR4, OCIF-DDD1 and OCIF-DDD2 were designated as pCEP4-OCIF-DCR1, pCEP4-OCIF-DCR2, pCEP4-OCIF-DCR3, pCEP4-OCIF-DCR4, pCEP4-OCIF-DDD1 and pCEP4-OCIF-DDD2, respectively.

iii) Preparation of OCIF with C-terminal domain truncation

(1) mutagenesis of OCIF cDNA

A series of OCIF mutants with deletions of from Cys at amino acid residue 379 to Leu 380, from Ser 331 to Leu 380, from Asp 252 to Leu 380, from Asp 177 to Leu 380, from Arg 123 to Leu 380 and from Cys 86 to Leu 380 was prepared. Positions of the amino acid residues are shown in SEQUENCE NO: 4. These mutants were designated as OCIF-CL, OCIF-CC, OCIF-CDD2, OCIF-CDD1, OCIF-CCR4 and OCIF-CCR3, respectively.

Mutagenesis for OCIF-CL was performed by the two-step PCR as described in EXAMPLE 22-(ii). The primer set for the reaction is shown in Table 12. The nucleotide sequences of the primers are shown in SEQUENCE NO:23, 40, 55, and 56. The final PCR products were precipitated with ethanol, dried under vacuum and dissolved in 40 μ l of sterile distilled water. This DNA solution was designated as solution L.

The DNA fragment which is contained in solution L (20 μ l) was digested with restriction enzymes BstP I and EcoR. A DNA fragment with an approximate size of 100 bp was extracted from a preparative agarose gel with QIAEX gel extraction kit and dissolved in 20 μ l of sterile distilled water. This DNA solution was designated as DNA solution 19. Two microliters of DNA solution 19, 3 μ l of DNA solution 10 (described in EXAMPLE 22-(ii)) and 5 μ l of ligation buffer I of DNA ligation kit ver. 2 were mixed and ligation reaction was carried out. Competent *E. coli* DH5 α cells were transformed with 5 μ l of the ligation mixture. Ampicillin-resistant transformants were screened for a clone containing a plasmid DNA. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmid thus obtained was named pSK-OCIF-CL. Mutagenesis of OCIF cDNA to prepare OCIF-CC, OCIF-CDD2, OCIF-CDD1, OCIF-CCR4 and OCIF-CCR3 was performed by a one-step PCR.

PCR reactions for mutagenesis to prepare OCIF-CC, OCIF-CDD2, OCIF-CDD1, OCIF-CCR4 and OCIF-CCR3

10X Ex Taq Buffer (Takara Shuzo)	10 μ l
2.5 mM solution of dNTPs	8 μ l
the plasmid vector containing the entire OCIF cDNA described in EXAMPLE 11 (8ng/ml)	2 μ l
sterile distilled water	73.5 μ l
20 μ M solution of primer OCIF Xho F	5 μ l
100 μ M solution of primer (for mutagenesis)	1 μ l
Ex Taq (Takara Shuzo)	0.5 μ l

Table 12

mutants	primer-1	primer-2	primer-3	primer-4
OCIF-CL	IF 6	CL R	IF 14	CL F

Specific primers were used for each mutagenesis and other components were unchanged.

Primers used for the mutagenesis are shown in Table 13. Their nucleotide sequences are shown in SEQUENCE NO:57-61. The components of each PCR were mixed in a microcentrifuge tube and PCR was performed as follows. The microcentrifuge tubes were treated for 3 minutes at 97 °C and then incubated sequentially, for 30 seconds at 95 °C, 30 seconds at 50 °C and 3 minutes at 70 °C. This three-step incubation procedure was repeated 25 times, and after that, the tubes were incubated for 5 minutes at 70 °C. An aliquot of the reaction mixture was removed from each tube and analyzed by an agarose gel electrophoresis to confirm the size of each product.

The size of the PCR products was confirmed on an agarose gel. Excess primers in the PCRs were removed using Amicon microcon (Amicon) after completion of the reaction. The DNA fragments were precipitated with ethanol, dried under vacuum and dissolved in 40 μ l of sterile distilled water. The DNA fragment in each DNA solution was digested with restriction enzymes Xho I and Bam HI. After the reactions, DNA was precipitated with ethanol, dried under vacuum and dissolved in 20 μ l of sterile distilled water.

The solutions containing DNA fragment with the CC deletion, the CDD2 deletion, the CDD1 deletion, the CCR4 deletion and the CCR3 deletion were designated as CC DNA solution, CDD2 DNA solution, CDD1 DNA solution, CCR4 DNA solution and CC R3 DNA solution, respectively.

Table 13

mutants	primers for the mutagenesis
OCIF-CC	CC R
OCIF-CDD2	CDD2 R
OCIF-CDD1	CDD1 R
OCIF-CCR4	CCR4 R
OCIF-CCR3	CCR3 R

(2) Construction of vectors for expressing the OCIF mutants

pSK-OCIF-CL was digested with restriction enzymes Bam HI and Xho I. The Bam HI-Xho I DNA fragment containing the entire coding sequence for OCIF-CL was isolated and dissolved in 20 μ l of sterile distilled water. This DNA solution was designated as CL DNA solution. One microliter of pCEP 4 DNA solution and 6 μ l of either of CL DNA solution, CC DNA solution, CDD2 DNA solution, CDD1 DNA solution, CCR4 DNA solution or CCR3 DNA solution were independently mixed with 7 μ l of ligation buffer I of DNA ligation kit ver. 2 and ligation reactions were carried out. Competent

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E. coli DH5 α cells (100 μ l) were transformed with 7 μ l of each ligation mixture. Ampicillin-resistant transformants were screened for clones containing plasmids which have the desirable mutations in OCIF cDNA by analyzing the DNA structure. In each plasmid, OCIF cDNA fragment having a deletion were inserted between the recognition sites of Xho I and Bam HI of pCEP 4. The plasmids containing the cDNA encoding OCIF-CL, OCIF-CC, OCIF-CDD1, OCIF-CDD2, OCIF-CCR4 and OCIF-CCR3 were designated pCEP4-OCIF-CL, pCEP4-OCIF-CC, pCEP4-OCIF-CDD2, pCEP4-OCIF-CDD1, pCEP4-OCIF-CCR4 and pCEP4-OCIF-CCR3, respectively.

iv) Preparation of OCIF mutants with C-terminal truncation

(1) Introduction of C-terminal truncation to OCIF

A series of OCIF mutants with C-terminal truncation was prepared. OCIF mutant in which 10 residues of from Gln at 371 to Leu at 380 are replaced with 2 residues of Leu-Val was designated OCIF-CBst. OCIF mutant in which 83 residues of from Cys 298 to Leu 380 are replaced with 3 residues of Ser-Leu-Asp was designated OCIF-CSph. OCIF mutant in which 214 residues of from Asn 167 to Leu 380 are removed was designated OCIF-CBsp. OCIF mutant in which 319 residues of from Asp 62 to Leu 380 are replaced with 2 residues of Leu-Val was designated OCIF-CPst. Positions of the amino acid residues are shown in SEQUENCE NO: 4.

Two micrograms each of pSK + -OCIF was digested with one of the restriction enzymes, Bst PI, Sph I, PstI (Takara Shuzo), and Bsp EI (New England Biolabs), and followed by phenol extraction and ethanol precipitation. The precipitated DNA was dissolved in 10 μ l of sterile distilled water. Ends of the DNAs in 2 μ l of each solution were blunted using a DNA blunting kit in final volumes of 5 μ l. To the reaction mixtures, 1 μ g (1 μ l) of an Amber codon-containing Xba I linker (5'-CTAGTCTAGACTAG-3') and 6 μ l of ligation buffer I of DNA ligation kit ver. 2 were added.

After the ligation reactions, 6 μ l each of the reaction mixtures was used to transform *E. coli* DH5 α . Ampicillin-resistant transformants were screened for clones containing plasmids. DNA structure was analyzed by restriction enzyme mapping and by DNA sequencing. The plasmids thus obtained were named pSK-OCIF-CBst, pSK-OCIF-CSph, pSK-OCIF-CBsp and pSK-OCIF-CPst, respectively.

(2) Construction of vectors for expressing the OCIF mutants

pSK-OCIF-CBst, pSK-OCIF-CSph, pSK-OCIF-CBsp and pSK-OCIF-CPst were digested with restriction enzymes Bam HI and Xho I. The 1.5 kb of DNA fragment containing entire coding sequence for each OCIF mutant was isolated and dissolved in 20 μ l of sterile distilled water. These DNA solutions that contain the Bam HI-XhoI fragment derived from pSK-OCIF-CBst, pSK-OCIF-CSph, pSK-OCIF-CBsp and pSK-OCIF-CPst were designated as CBst DNA solution, CSph DNA solution, CBsp DNA solution and CPst DNA solution, respectively. One microliter of pCEP 4 DNA solution (described in EXAMPLE 22-ii) and 6 μ l of either CBst DNA solution, CSph DNA solution, CBsp DNA solution or CPst DNA solution were independently mixed with 7 μ l of ligation buffer I of DNA ligation kit ver. 2 and ligation reactions were carried out. Competent *E. coli* DH5 α cells (100 μ l) were transformed with 7 μ l of each ligation mixture. Ampicillin-resistant transformants were screened for clones containing plasmids in which cDNA fragment is inserted between the recognition sites of Bam HI and Xho I of pCEP 4 by analyzing the DNA structure. The plasmids containing the cDNA encoding OCIF-CBst, OCIF-CSph, OCIF-CBsp and OCIF-CPst were designated as pCEP4-OCIF-CBst, pCEP4-OCIF-CSph, pCEP4-OCIF-CBsp and pCEP4-OCIF-CPst, respectively.

v) Preparation of vectors for expressing the OCIF mutants

E. coli clones harboring the expression vectors for OCIF mutants (total of 21 clones) were grown and the vectors were purified by QIAGEN column (QIAGEN). All the expression vectors were precipitated with ethanol and dissolved in appropriate volumes of sterile distilled water and used for further manipulations shown below.

vi) Transient expression of the cDNAs for OCIF mutants and biological activities of the mutants

OCIF mutants were produced using the expression vectors prepared in EXAMPLE 22-v). The method was essentially the same as described in EXAMPLE 13. Only the modified points are described below. A 24-well plate was used for the DNA transfection. 2×10^5 cells of 293/EBNA suspended in IMDM containing 10% fetal bovine serum were seeded into each well of the plate. One microgram of purified vector DNA and 4 μ l of lipofectamine were used for each transfection. Mixture of an expression vector and lipofectamine in OPTI-MEM (GIBCO BRL) in a final volume of 0.5 ml was added to the cells in a well. After the cells were incubated at 37°C for 24 hr in a CO₂ incubator, the medium was replaced with 0.5 ml of Ex-cell 301 medium (JSR). The cells were incubated at 37°C for 48 more hours in the CO₂ incubator. The conditioned medium was collected and used for assay for in vitro biological activity. The nucleotide

sequences of cDNAs for the OCIF mutants are shown in SEQUENCE NO:83-103. The deduced amino acid sequences for the OCIF mutants are shown in SEQUENCE NO: 62-82. The assay for in vitro biological activity was performed as described in EXAMPLE 13. Antigen concentration of each conditioned medium was determined by ELISA as described in EXAMPLE 24. Table 14 shows specific activity of the mutants relative to that of the unaltered OCIF.

Table 14

mutants	activity
the unaltered OIF	++
OCIF-C19S	+
OCIF-C20S	±
OCIF-C21S	±
OCIF-C22S	+
OCIF-C23S	++
OCIF-DCR1	±
OCIF-DCR2	±
OCIF-DCR3	±
OCIF-DCR4	±
OCIF-DDD1	+
OCIF-DDD2	±
OCIF-CL	++
OCIF-CC	++
OCIF-CDD2	++
OCIF-CDD1	+
OCIF-CCR4	±
OCIF-CCR3	±
OCIF-CBst	++
OCIF-CSph	++
OCIF-CBsp	±
OCIF-CPst	±
++ indicates relative activity more than 50% of that of the unaltered OCIF + indicates relative activity between 10% and 50% ± indicates relative activity less than 10%, or production level too low to determine the accurate biological activity	

vii) western blot analysis

Ten microliters of the final conditioned medium was used for western blot analysis. Ten microliters of the sample were mixed with 10 µl of SDS-PAGE sample buffer (0.5 M Tris-HCl, 20% glycerol, 4% SDS, 20µg/ml bromo phenol blue, pH 6.8) boiled for 3 min. and subjected to a 10 % SDS polyacryl amide gel electrophoresis under non-reducing conditions. After the electrophoresis, the separated proteins were blotted to PVDF membrane (ProBlott[®], Perkin Elmer) using a semi-dry electroblotter (BIO-RAD). The membrane was incubated at 37°C with horseradish peroxidase labeled anti-OCIF antibodies for 2 hr. After the membrane was washed, protein bands which react with the labeled antibodies were detected using ECL system (Amersham). Two protein bands with approximate molecular masses of 60kD and 120kD were detected for the unaltered OCIF. On the other hand, almost exclusively 60kD protein band was detected for OCIF-C23S, OCIF-CL and OCIF CC. Protein bands with an approximate masses of 40kD-50kD and 30kD-40kD were the major ones for OCIF-CDD2 and OCIF-CDD1, respectively. These results indicate that Cys at 379 is responsible for the dimer formation, both the monomers and the dimers maintain the biological activity and a deletion of residues from Asp

at 177 to Leu at 380 does not abolish the biological activity of OCIF (positions of the amino acid residue shown in SEQUENCE NO: 4).

EXAMPLE 23

Isolation of human genomic OCIF gene

i) Screening of a human genomic library

An amplified human placenta genomic library in Lambda FIX II vector purchased from STRATAGENE was screened for the gene encoding human OCIF using the human OCIF cDNA as a probe. Essentially, screening was done according to the instruction manual supplied with the genomic library. The basic protocols described in Molecular Cloning: A Laboratory Manual also were employed to manipulate phage, *E. coli*, and DNA.

The library was titrated, and 1×10^6 pfu of phage was mixed with XL1-Blue MRA host *E. coli* cells and plated on 20 plates (9 cm x 13 cm) with 9 ml per plate of top agarose. The plates were incubated overnight at 37°C. Filter plaque lifts were prepared using Hybond-N nylon membranes (Amersham). The membranes were processed by denaturation in a solution containing 1.5 M NaCl and 0.5 M NaOH for 1 minute at room temperature. The membranes were then neutralized by placing successively for one minute each in 1 M Tris-HCl (pH 7.5) and a solution containing 1.5 M NaCl and 0.5 M Tris-HCl (pH 7.5). The membranes were then transferred onto a filter paper wet with 2xSSC. Phage DNA was fixed on the membranes with 1200 μJoules of UV energy in STRATALINKER UV crosslinker 2400 (STRATAGENE) and the membranes were air dried. The membranes were immersed in Rapid Hybridization buffer (Amersham) and incubated for one hour at 65 °C before hybridization with ^{32}P -labeled cDNA probe in the same buffer overnight at 65°C. Screening probe was prepared by labeling the OCIF cDNA with ^{32}P using the Megaprime DNA labeling system (Amersham). Approximately, 5×10^5 cpm probe was used for each ml of hybridization buffer. After the hybridization, the membranes were rinsed in 2xSSC for five minutes at room temperature. The membranes were then washed four times, 20 minutes each time, in 0.5xSSC containing 0.1 % SDS at 65 °C. After the final wash, the membranes were dried and subjected to autoradiography at -80 °C with SUPER HR-H X-ray film (FUJI PHOTO FILM Co., Ltd.) and an intensifying screen. Upon examination of the autoradiograms, six positive signals were detected. Agar plugs were picked from the regions corresponded to these signals for phage purification. Each agar plug was soaked overnight in 0.5 ml of SM buffer containing 1% chloroform to extract phage. Each extract containing phage was diluted 1000 fold with SM buffer and an aliquot of 1 ml or 20 ml was mixed with host *E. coli* described above. The mixture was plated on agar plates with top agarose as described above. The plates were incubated overnight at 37 °C, and filter lifts were prepared, prehybridized, hybridized, washed and autoradiographed as described above. This process of phage purification was applied to all six positive signals initially detected on the autoradiograms and was repeated until all phage plaques on agar plates hybridize with the cDNA probe. After purification, agar plugs of each phage isolate were soaked in SM buffer containing 1% chloroform and stored at 4 °C. Six individual phage isolates were designated λOIF3, λOIF8, λOIF9, λOIF11, λOIF12 and λOIF17, respectively.

ii) Analysis of the genomic clones by restriction enzyme digestion and Southern blot hybridization

DNA was prepared from each phage isolate by the plate lysate method as described in Molecular Cloning: A Laboratory Manual. DNA prepared from each phage was digested with restriction enzymes and the fragments derived from the digestion were separated on agarose gels. The fragments were then transferred to nylon membranes and subjected to Southern blot hybridization using OCIF cDNA as a probe. The results of the analysis revealed that the six phage isolates are individual clones. Among these fragments derived from the restriction enzyme digestion, those fragments which hybridized with the OCIF cDNA probe were subcloned into plasmid vectors and subjected to the nucleotide sequence analysis as described below.

iii) Subcloning restriction fragments derived from genomic clones into plasmid vectors and determination of the nucleotide sequence.

λOIF8 DNA was digested with restriction enzymes EcoRI and NotI, and the DNA fragments derived these from were separated on a 0.7% agarose gel. The 5.8 kilobase pairs (kb) EcoRI/NotI fragment was extracted from the gel using QIAEX II Gel Extraction Kit (QIAGEN) according to the procedure recommended by the manufacturer. The 5.8 kb EcoRI/NotI fragment was ligated with pBluescript II SK+ vector (STRATAGENE) which had been linearized with restriction enzymes EcoRI and NotI, using Ready-To-Go T4 DNA Ligase (Pharmacia) according to the procedure recommended by the manufacturer. Competent DH5 α *E. coli* cells (Amersham) were transformed with the recombinant plasmid and transformants were selected on L-plates containing 50 μg/ml of ampicillin. A clone harboring the recom-

EXAMPLE 26

Therapeutic effect on osteoporosis

5 (1) Method

Male Fischer rats, 6 weeks-old, were subjected to denervation of left forelimb. These rats were assigned to four groups (10 rats/group) and treated as follows ; group A, sham operated rats without administration ; group B, denervated rats with intravenous administration of vehicle ; group C, denervated rats administered OCIF intravenously at a dose of 5 µg/kg twice a day ; group D, denervated rats administered OCIF intravenously at a dose of 50 µg/kg twice a day. After denervation, OCIF was administered daily for 14 days. After 2 weeks treatment, the animals were sacrificed and their forelimbs were dissected. Thereafter bones were tested for mechanical strength.

(2) Results

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Decrease of bone strength was observed in the animals of control groups as compared to those animals of the normal groups while bone strength was increase in the groups of animal received 50 mg of OCIF per kg body weight.

Industrial availability

20

The present invention provides both a novel protein which inhibits formation of osteoclasts and a efficient procedure to produce the protein. The protein of the present invention has an activity to inhibit formation of osteoclasts. The protein will be useful for the treatment of many diseases accompanying bone loss, such as osteoporosis, and as an antigen to be used for the immunological diagnosis of such diseases.

25

Referring to the deposited the microorganism

Name and Address of the Depositary Authority

30

Name: National Institute of Bioscience and Human-Technology Agency of Industrial Science and Technology Ministry of International Trade and Industry

Address: 1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki-ken 305, JAPAN

Deposited date: June 21, 1995

(It was transferred from Bikkoken No. P-14998, which was deposited on June 21, 1995.

35

Transferred date: October 25, 1995)

Acession Number: FERM BP-5267

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45

50

55

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: SNOW BRANDS MILK PRODUCTS CO., LTD.

(B) STREET:

(C) CITY:

(D) STATE:

(E) COUNTRY:

(F) POSTAL CODE (ZIP):

(G) TELEPHONE:

(H) TELEFAX:

(I) TELEX:

(ii) TITLE OF INVENTION: Novel proteins and methods for producing the
proteins

(iii) NUMBER OF SEQUENCES: 105

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER:

(C) OPERATING SYSTEM:

(D) SOFTWARE: Wordperfect windows

(v) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: JP

(B) FILE REFERENCE:

(C) FILING DATE:

(2) INFORMATION FOR SEQUENCE ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 6

(B) TYPE : amino acid

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : peptide (an internal amino acid sequence of the protein)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 1:

Xaa Tyr His Phe Pro Lys

1 5

(2) INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 14

(B) TYPE : amino acid

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : peptide (an internal amino acid sequence of the protein)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO:2:

Xaa Gln His Ser Xaa Gln Glu Gln Thr Phe Gln Leu Xaa Lys

1 5 10

(2) INFORMATION FOR SEQUENCE ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 12

(B) TYPE : amino acid

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : peptide (an internal amino acid sequence of the protein)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 3:

Xaa Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys

1 5 10

(2) INFORMATION FOR SEQUENCE ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 380

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(B) TYPE : amino acid

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF protein without signal peptide)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO:4:

	Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser	
	1 5 10 15	
10	His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys	
	20 25 30	
	Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro	
15	35 40 45	
	Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu	
	50 55 60	
20	Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu	
	65 70 75	
	Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg	
	80 85 90	
25	Tyr Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro	
	95 100 105	
	Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val	
30	110 115 120	
	Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser	
	125 130 135	
	Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu	
35	140 145 150	
	Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser	
	155 160 165	
40	Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu	
	170 175 180	
	Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr	
	185 190 195	
45	Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys	
	200 205 210	
	Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser	
	215 220 225	
50	Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn	
	230 235 240	

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Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu
245 250 255
Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr
260 265 270
Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys
275 280 285
Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro
290 295 300
Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
305 310 315
Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His
320 325 330
Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys
335 340 345
Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr
350 355 360
Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val
365 370 375
Lys Ile Ser Cys Leu
380

(2) INFORMATION FOR SEQUENCE ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 401

(B) TYPE : amino acid

(D) TOPOLOGY.: linear

(ii) MOLECULE TYPE : protein (OCIF protein with signal peptide)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 5:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
-20 -15 -10
Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
-5 -1 1 5
Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
10 15 20
Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
25 30 35
Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His

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	40	45	50
5	Thr Ser Asp Glu Cys	Leu Tyr Cys Ser Pro	Val Cys Lys Glu Leu
	55	60	65
	Gln Tyr Val Lys Gln	Glu Cys Asn Arg Thr	His Asn Arg Val Cys
	70	75	80
10	Glu Cys Lys Glu Gly	Arg Tyr Leu Glu Ile	Glu Phe Cys Leu Lys
	85	90	95
	His Arg Ser Cys Pro	Pro Gly Phe Gly Val	Val Gln Ala Gly Thr
	100	105	110
15	Pro Glu Arg Asn Thr	Val Cys Lys Arg Cys	Pro Asp Gly Phe Phe
	115	120	125
	Ser Asn Glu Thr Ser	Ser Lys Ala Pro Cys	Arg Lys His Thr Asn
20	130	135	140
	Cys Ser Val Phe Gly	Leu Leu Leu Thr Gln	Lys Gly Asn Ala Thr
	145	150	155
	His Asp Asn Ile Cys	Ser Gly Asn Ser Glu	Ser Thr Gln Lys Cys
25	160	165	170
	Gly Ile Asp Val Thr	Leu Cys Glu Glu Ala	Phe Phe Arg Phe Ala
	175	180	185
30	Val Pro Thr Lys Phe	Thr Pro Asn Trp Leu	Ser Val Leu Val Asp
	190	195	200
	Asn Leu Pro Gly Thr	Lys Val Asn Ala Glu	Ser Val Glu Arg Ile
	205	210	215
35	Lys Arg Gln His Ser	Ser Gln Glu Gln Thr	Phe Gln Leu Leu Lys
	220	225	230
	Leu Trp Lys His Gln	Asn Lys Asp Gln Asp	Ile Val Lys Lys Ile
40	235	240	245
	Ile Gln Asp Ile Asp	Leu Cys Glu Asn Ser	Val Gln Arg His Ile
	250	255	260
	Gly His Ala Asn Leu	Thr Phe Glu Gln Leu	Arg Ser Leu Met Glu
45	265	270	275
	Ser Leu Pro Gly Lys	Lys Val Gly Ala Glu	Asp Ile Glu Lys Thr
	280	285	290
50	Ile Lys Ala Cys Lys	Pro Ser Asp Gln Ile	Leu Lys Leu Leu Ser
	295	300	305
	Leu Trp Arg Ile Lys	Asn Gly Asp Gln Asp	Thr Leu Lys Gly Leu

55

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310 315 320
Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr
5 325 330 335
Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe
340 345 350
10 Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly
355 360 365
Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
370 375 380
15

(2) INFORMATION FOR SEQUENCE ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH : 1206
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear
25

(ii) MOLECULE TYPE : cDNA (OCIF)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 6:

30 ATGAACAACCT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
TGIGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
GTGTGCGCCC CTGCCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
35 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCGAGA GCGAAATACA 420
40 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT 480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC 600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660
45 AGTGTCTTGG TAGACAATTI GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAAACAGC 840
50 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA 960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAATGG CGACCAAGAC 1020
55

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ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAACT 1080
 5 GTCACCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG 1140
 TATCAGAAGT TATTTT TAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC 1200
 TTATAA 1206

(2) INFORMATION FOR SEQUENCE ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 15

(B) TYPE : amino acid

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : peptide (a N-terminal amino acid sequence of the protein)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO:7:

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser
 1 5 10 15

(2) INFORMATION FOR SEQUENCE NO ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 1185

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF2)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO:8

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 40 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGTGC AATCGCACCC ACAACCGCGT GTGCGAATGC 300
 AAGGAAGGGC GCTACCTTGA GATAGAGTTC TGCTTGAAAC ATAGGAGCTG CCTCCTGGA 360
 45 TTTGGAGTGG TGCAAGCTGG AACCCAGAG CGAAATACAG TTTGCAAAAG ATGTCCAGAT 420
 GGGTTCTTCT CAAATGAGAC GTCATCTAAA GCACCCTGTA GAAAACACAC AAATTGCAGT 480
 GTCTTTGGTC TCCTGCTAAC TCAGAAAGGA AATGCAACAC ACGACAACAT ATGTTCCGGA 540
 AACAGTGAAT CAACTCAAAA ATGTGGAATA GATGTTACCC TGTGTGAGGA GGCATTCTTC 600
 50 AGGTTTGCTG TTCCTACAAA GTTTACGCCT AACTGGCTTA GTGTCTTGGT AGACAATTTG 660
 CCTGGCACCA AAGTAAACGC AGAGAGTGTA GAGAGGATAA AACGGCAACA CAGCTCACAA 720

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GAACAGACTT TCCAGCTGCT GAAGTTATGG AAACATCAAA ACAAAGACCA AGATATAGTC 780
 AAGAAGATCA TCCAAGATAT TGACCTCTGT GAAAACAGCG TGCAGCGGCA CATTGGACAT 840
 GCTAACCTCA CCTTCGAGCA GCTTCGTAGC TTGATGGAAA GCTTACCGGG AAAGAAAGTG 900
 GGAGCAGAAG ACATTGAAAA AACAATAAAG GCATGCAAAC CCAGTGACCA GATCCTGAAG 960
 CTGCTCAGTT TGTGGCGAAT AAAAAATGGC GACCAAGACA CCTTGAAGGG CCTAATGCAC 1020
 GCACTAAAGC ACTCAAAGAC GTACCACTTT CCCAAACTG TCACTCAGAG TCTAAAGAAG 1080
 ACCATCAGGT TCCTTCACAG CTTACAATG TACAAATTGT ATCAGAAGTT ATTTTGTAGAA 1140
 ATGATAGGTA ACCAGGTCCA ATCAGTAAAA ATAAGCTGCT TATAA 1185

(2) INFORMATION FOR SEQUENCE ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 394

(B) TYPE : amino acid

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF2)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser
-20							-15					-10		
Ile	Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His
-5					-1	1					5			
Tyr	Asp	Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro
10					15					20				
Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr
25					30					35				
Val	Cys	Ala	Pro	Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His
40					45					50				
Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Cys
55					60					65				
Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr
70					75					80				
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly
85					90					95				
Phe	Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys
100					105					110				
Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys
115					120					125				

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	Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu	
	130	140
5	Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly	
	145	155
	Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys	
10	160	170
	Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro	
	175	185
	Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val	
15	190	200
	Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln	
	205	215
20	Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys	
	220	230
	Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys	
	235	245
25	Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe	
	250	260
	Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val	
30	265	275
	Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser	
	280	290
	Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly	
35	295	305
	Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser	
	310	320
40	Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys	
	325	335
	Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln	
	340	350
45	Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys	
	355	365
	Ile Ser Cys Leu	
50	370	373

(2) INFORMATION FOR SEQUENCE ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 1089

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF3)

(xi) SEQUENCE DESCRIPTION ID NO: 10:

ATGAACAAGT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGTACCTTG AGATAGAGTT CTGCTTGAAG 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCGAGA GCGAAATACA 420
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT 480
 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC 600
 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC AGTTTGTGGC GAATAAAAAA TGGCGACCAA 900
 GACACCTTGA AGGGCCTAAT GCACGCACTA AAGCACTCAA AGACGTACCA CTTTCCCAAA 960
 ACTGTCACTC AGAGTCTAAA GAAGACCATC AGGTTCTTTC ACAGCTTCAC AATGTACAAA 1020
 TTGTATCAGA AGTTATTTTT AGAAATGATA GGTAACCAGG TCCAATCAGT AAAAATAAGC 1080
 TGCTTATAA 1089

(2) INFORMATION FOR SEQUENCE ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 362

(B) TYPE : amino acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser

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	-20	-15	-10
	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His		
5	-5	-1 1	5
	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro		
	10	15	20
10	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr		
	25	30	35
	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His		
	40	45	50
15	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu		
	55	60	65
	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys		
	70	75	80
20	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys		
	85	90	95
	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr		
25	100	105	110
	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe		
	115	120	125
30	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn		
	130	135	140
	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr		
	145	150	155
35	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys		
	160	165	170
	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala		
	175	180	185
40	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp		
	190	195	200
	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile		
45	205	210	215
	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys		
	220	225	230
50	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile		
	235	240	245
	Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile		

55

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250 255 260
 Gly His Ala Asn Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln
 5 265 270 275
 Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr
 280 285 290
 10 Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile
 295 300 305
 Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu
 310 315 320
 15 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser
 325 330 335
 Cys Leu
 20 340 341

(2) INFORMATION FOR SEQUENCE ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH : 465
 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 30 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF4)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 12:

ATGAACAAGT TGCTGTGCTG CTCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 35 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 40 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTGGAGTG GTGCAAGCTG GTACGTGTCA ATGTGCAGCA 420
 AAATTAATTA GGATCATGCA AAGTCAGATA GTTGTGACAG TTTAG 465

(2) INFORMATION FOR SEQUENCE ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH :154
 (B) TYPE : amino acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF4)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

Met Asn Lys Leu Leu Cys Cys Ser Leu Val Phe Leu Asp Ile Ser
-20          -15          -0
Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
-5          -1   1          5
Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
10          15          20
Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
25          30          35
Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
40          45          50
Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
55          60          65
Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
70          75          80
Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
85          90          95
His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
100         105         110
Cys Gln Cys Ala Ala Lys Leu Ile Arg Ile Met Gln Ser Gln Ile
115         120         125
Val Val Thr Val
130         133

```

(2) INFORMATION FOR SEQUENCE ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 438

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF5)

(xi) SEQUENCE DESCRIPTION ID NO: 14:

ATGAACAAGT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60

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CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GATGCAGGAG AAGACCCAAG 420
 CCACAGATAT GTATCTGA 438

(2) INFORMATION FOR SEQUENCE ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 140

(B) TYPE : amino acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF5)

(xi) SEQUENCE DESCRIPTION: ID NO: 15:

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 -5 -1 1 5
 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 10 15 20
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 25 30 35
 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
 40 45 50
 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
 55 60 65
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
 70 75 80
 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
 85 90 95
 His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Cys
 100 105 110
 Arg Arg Arg Pro Lys Pro Gln Ile Cys Ile
 115 120 124

(2) INFORMATION FOR SEQUENCE ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 20
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer T3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

AATTAACCCT CACTAAAGGG

20

(2) INFORMATION FOR SEQUENCE ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 22
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer T7)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GTAATACGAC TCACTATAGG GC

22

(2) INFORMATION FOR SEQUENCE ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 20
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF1)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 18:

ACATCAAAAC AAAGACCAAG

20

(2) INFORMATION FOR SEQUENCE ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 20
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF2)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 19:

TCTTGGTCTT TGTTTTGATG

20

(2) INFORMATION FOR SEQUENCE ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 20

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF3)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 20:

TTATTCGCCA CAACTGAGC

20

(2) INFORMATION FOR SEQUENCE ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 20

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF4)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 21:

TTGTGAAGCT GTGAAGGAAC

20

(2) INFORMATION FOR SEQUENCE ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 20

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF5)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 22:

GCTCAGTTTG TGGCGAATAA

20

(2) INFORMATION FOR SEQUENCE ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 20
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF6)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 23:

GTGGGAGCAG AAGACATTGA

20

(2) INFORMATION FOR SEQUENCE ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 20
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF7)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 24:

AATGAACAAC TTGCTGTGCT

20

(2) INFORMATION FOR SEQUENCE ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 20
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF8)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 25:

TGACAAATGT CCTCCTGGTA

20

(2) INFORMATION FOR SEQUENCE ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 20
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF9)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 26:

AGGTAGGTAC CAGGAGGACA

20

(2) INFORMATION FOR SEQUENCE ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 20

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF10)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 27:

GAGCTGCCCT CCTGGATTG

20

(2) INFORMATION FOR SEQUENCE ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 20

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF11)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 28:

CAAACTGTAT TTCGCTCTGG

20

(2) INFORMATION FOR SEQUENCE ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 20

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF12)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 29:

GTGTGAGGAG GCATTCTTCA

20

(2) INFORMATION FOR SEQUENCE ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 32

(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer C19SF)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 30:

GAATCAACTC AAAAAAGTGG AATAGATGTT AC

32

(2) INFORMATION FOR SEQUENCE ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 32
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer C19SR)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 31:

GTAACATCTA TTCCACTTTT TTGAGTTGAT TC

32

(2) INFORMATION FOR SEQUENCE ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 30
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer C20SF)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 32:

ATAGATGTTA CCCTGAGTGA GGAGGCATTC

30

(2) INFORMATION FOR SEQUENCE ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 30
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer C20SR)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 33:

GAATGCCTCC TCACTCAGGG TAACATCTAT

30

5 (2) INFORMATION FOR SEQUENCE ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 31

10 (B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer C21SF)

15 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 34:

CAAGATATTG ACCTCAGTGA AAACAGCGTG C

31

20 (2) INFORMATION FOR SEQUENCE ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 31

25 (B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer C21SR)

30 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 35:

GCACGCTGTT TTCACTGAGG GCAATATCTT G

31

35 (2) INFORMATION FOR SEQUENCE ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 31

(B) TYPE : nucleic acid

40 (C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer C22SF)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 36:

45 AAAACAATAA AGGCAAGCAA ACCCAGTGAC C

31

(2) INFORMATION FOR SEQUENCE ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH : 31

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single
 (D) TOPOLOGY : linear
 5 (ii) MOLECULE TYPE : synthetic DNA (primer C22SR)
 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 37:
 GGTCAC TGGG TTGCTTGCC TTTATTGTTT T 31

10 (2) INFORMATION FOR SEQUENCE ID NO: 38:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH : 31
 15 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear
 20 (ii) MOLECULE TYPE : synthetic DNA (primer C23SF)
 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 38:
 TCAGTAAAAA TAAGCAGCTT ATAAGTGGCC A 31

25 (2) INFORMATION FOR SEQUENCE ID NO: 39:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH : 31
 30 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear
 35 (ii) MOLECULE TYPE : synthetic DNA (primer C23SR)
 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 39:
 TGGCCAGTTA TAAGCTGCTT ATTTTACTG A 31

40 (2) INFORMATION FOR SEQUENCE ID NO: 40:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH : 22
 45 (B) TYPE : nucleic acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear
 50 (ii) MOLECULE TYPE : synthetic DNA (primer IF 14)
 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 40:
 TTGGGGTTTA TTGAGGAGA TG 22

55

(2) INFORMATION FOR SEQUENCE ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 36

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer DCR1F)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 41:

ACCACCCAGG AACCTTGCCC TGACCACTAC TACACA

36

(2) INFORMATION FOR SEQUENCE ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 36

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer DCR1R)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 42:

GTGAGGGCAA GGTTCCTGGG TGGTCCAATT AATGGA

36

(2) INFORMATION FOR SEQUENCE ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 36

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer DCR2F)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 43:

ACCGTGTGCG CCGAATGCAA GGAAGGGCGC TACCTT

36

(2) INFORMATION FOR SEQUENCE ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 36

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer DCR2R)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 44:

TTCCTTGCAT TCGGCGCACA CCGTCTTCCA CTTTGC

36

(2) INFORMATION FOR SEQUENCE ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 36

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer DCR3F)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 45:

AACCGCGTGT GCAGATGTCC AGATGGGTTC TTCTCA

36

(2) INFORMATION FOR SEQUENCE ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 36

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer DCR3R)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 46:

ATCTGGACAT CTGCACACGC GGTGTGGGT GCGATT

36

(2) INFORMATION FOR SEQUENCE ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 36

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer DCR4F)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 47:

ACAGTTTGCA AATCOGAAA CAGTGAATCA ACTCAA

36

(2) INFORMATION FOR SEQUENCE ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 36

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer DCR4R)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 48:

ACTGTTTCCG GATTGCAAA CTGTATTTCG CTCTGG

36

(2) INFORMATION FOR SEQUENCE ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 36

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer DDD1F)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 49:

AATGTGGAAT AGATATTGAC CTCTGTGAAA ACAGCG

36

(2) INFORMATION FOR SEQUENCE ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 36

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer DDD1R)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 50:

AGAGGTCAAT ATCTATTCCA CATTTTGTAG TTGATT

36

(2) INFORMATION FOR SEQUENCE ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 36

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer DDD2F)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 51:

AGATCATCCA AGACGCACTA AAGCACTCAA AGACGT

36

5

(2) INFORMATION FOR SEQUENCE ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 36

10

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer DDD2R)

15

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 52:

GCTTTAGTGC GTCTTGATG ATCTTCTTGA CTATAT

36

20

(2) INFORMATION FOR SEQUENCE ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 29

(B) TYPE : nucleic acid

25

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer XhoI F)

30

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 53:

GGCTCGAGCG CCCAGCCGCC GCCTCCAAG

29

35

(2) INFORMATION FOR SEQUENCE ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 20

(B) TYPE : nucleic acid

40

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer IF 16)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 54:

45

TTTGAGTGCT TTAGTGCGTG

20

50

(2) INFORMATION FOR SEQUENCE ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 30

(B) TYPE : nucleic acid

55

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer CL F)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 55:

TCAGTAAAAA TAAGCTAACT GGAAATGGCC

30

(2) INFORMATION FOR SEQUENCE ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 30

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer CL R)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 56:

GGCCATTTC AGTTAGCTTA TTTTACTGA

30

(2) INFORMATION FOR SEQUENCE ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 29

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer CC R)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 57:

CCGGATCCTC AGTGCTTTAG TGGCGTCAT

29

(2) INFORMATION FOR SEQUENCE ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 29

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer CCD2 R)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 58:

CCGGATCCTC ATTGGATGAT CTTCTTGAC

29

(2) INFORMATION FOR SEQUENCE ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 29
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer CCD1 R)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 59:

CCGGATCCTC ATATTCCACA TTTTGTGAGT

29

(2) INFORMATION FOR SEQUENCE ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 29
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer CCR4 R)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 60:

CCGGATCCTC ATTTGCAAAC TGTATTTCG

29

(2) INFORMATION FOR SEQUENCE ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 29
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : synthetic DNA (primer CCR3 R)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 61:

CCGGATCCTC ATTCGCACAC GCGGTTGTG

29

(2) INFORMATION FOR SEQUENCE ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 401
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

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(ii) MOLECULE TYPE : Protein (OCIF-C19S)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 62:

5	Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser	
	-20	-15 -10
	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His	
	-5	-1 1 5
10	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro	
	10	15 20
	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr	
15	25	30 35
	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His	
	40	45 50
20	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu	
	55	60 65
	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys	
	70	75 80
25	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys	
	85	90 95
	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr	
30	100	105 110
	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe	
	115	120 125
	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn	
35	130	135 140
	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr	
	145	150 155
40	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Ser	
	160	165 170
	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala	
	175	180 185
45	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp	
	190	195 200
	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile	
	205	210 215
50	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys	
	220	225 230

55

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5 Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile
 235 240 245
 Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile
 250 255 260
 10 Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu
 265 270 275
 Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr
 280 285 290
 15 Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser
 295 300 305
 Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu
 310 315 320
 20 Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr
 325 330 335
 Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe
 340 345 350
 25 Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly
 355 360 365
 Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
 30 370 375 380

(2) INFORMATION FOR SEQUENCE ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH : 401
 (B) TYPE : amino acid
 (C) STRANDEDNESS : single
 40 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-C20S)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 63:

45 Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 -5 -1 1 5
 50 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 10 15 20
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr

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	25	30	35
	Val Cys Ala Pro Cys	Pro Asp His Tyr Tyr	Thr Asp Ser Trp His
5	40	45	50
	Thr Ser Asp Glu Cys	Leu Tyr Cys Ser Pro	Val Cys Lys Glu Leu
	55	60	65
10	Gln Tyr Val Lys Gln	Glu Cys Asn Arg Thr	His Asn Arg Val Cys
	70	75	80
	Glu Cys Lys Glu Gly	Arg Tyr Leu Glu Ile	Glu Phe Cys Leu Lys
	85	90	95
15	His Arg Ser Cys Pro	Pro Gly Phe Gly Val	Val Gln Ala Gly Thr
	100	105	110
	Pro Glu Arg Asn Thr	Val Cys Lys Arg Cys	Pro Asp Gly Phe Phe
20	115	120	125
	Ser Asn Glu Thr Ser	Ser Lys Ala Pro Cys	Arg Lys His Thr Asn
	130	135	140
	Cys Ser Val Phe Gly	Leu Leu Leu Thr Gln	Lys Gly Asn Ala Thr
25	145	150	155
	His Asp Asn Ile Cys	Ser Gly Asn Ser Glu	Ser Thr Gln Lys Cys
	160	165	170
	Gly Ile Asp Val Thr	Leu Ser Glu Glu Ala	Phe Phe Arg Phe Ala
30	175	180	185
	Val Pro Thr Lys Phe	Thr Pro Asn Trp Leu	Ser Val Leu Val Asp
	190	195	200
35	Asn Leu Pro Gly Thr	Lys Val Asn Ala Glu	Ser Val Glu Arg Ile
	205	210	215
	Lys Arg Gln His Ser	Ser Gln Glu Gln Thr	Phe Gln Leu Leu Lys
	220	225	230
40	Leu Trp Lys His Gln	Asn Lys Asp Gln Asp	Ile Val Lys Lys Ile
	235	240	245
	Ile Gln Asp Ile Asp	Leu Cys Glu Asn Ser	Val Gln Arg His Ile
45	250	255	260
	Gly His Ala Asn Leu	Thr Phe Glu Gln Leu	Arg Ser Leu Met Glu
	265	270	275
	Ser Leu Pro Gly Lys	Lys Val Gly Ala Glu	Asp Ile Glu Lys Thr
50	280	285	290
	Ile Lys Ala Cys Lys	Pro Ser Asp Gln Ile	Leu Lys Leu Leu Ser

55

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295 300 305
 Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu
 5 310 315 320
 Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr
 325 330 335
 10 Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe
 340 345 350
 Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly
 355 360 365
 15 Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
 370 375 380

(2) INFORMATION FOR SEQUENCE ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 401

(B) TYPE : amino acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-C21S)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 64:

30 Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 35 -5 -1 1 5
 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 10 15 20
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 40 25 30 35
 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
 40 45 50
 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
 45 55 60 65
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
 70 75 80
 50 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
 85 90 95

55

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	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr	
	100	105 110
5	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe	
	115	120 125
	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn	
10	130	135 140
	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr	
	145	150 155
	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys	
15	160	165 170
	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala	
	175	180 185
	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp	
20	190	195 200
	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile	
	205	210 215
25	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys	
	220	225 230
	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile	
30	235	240 245
	Ile Gln Asp Ile Asp Leu Ser Glu Asn Ser Val Gln Arg His Ile	
	250	255 260
	Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu	
35	265	270 275
	Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr	
	280	285 290
	Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser	
40	295	300 305
	Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu	
	310	315 320
45	Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr	
	325	330 335
	Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe	
	340	345 350
50	Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly	
	355	360 365

55

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Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
370 375 380

(2) INFORMATION FOR SEQUENCE ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 401
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-C22S)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 65:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser
	-20					-15					-10			
Ile	Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His
	-5				-1	1					5			
Tyr	Asp	Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro
	10				15					20				
Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr
	25				30					35				
Val	Cys	Ala	Pro	Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His
	40				45					50				
Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu
	55				60					65				
Gln	Tyr	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys
	70				75					80				
Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys
	85				90					95				
His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr
	100				105					110				
Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe
	115				120					125				
Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn
	130				135					140				
Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr
	145				150					155				
His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys

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	160	165	170
	Gly Ile Asp Val Thr	Leu Cys Glu Glu Ala	Phe Phe Arg Phe Ala
5	175	180	185
	Val Pro Thr Lys Phe	Thr Pro Asn Trp Leu	Ser Val Leu Val Asp
	190	195	200
10	Asn Leu Pro Gly Thr	Lys Val Asn Ala Glu	Ser Val Glu Arg Ile
	205	210	215
	Lys Arg Gln His Ser	Ser Gln Glu Gln Thr	Phe Gln Leu Leu Lys
	220	225	230
15	Leu Trp Lys His Gln	Asn Lys Asp Gln Asp	Ile Val Lys Lys Ile
	235	240	245
	Ile Gln Asp Ile Asp	Leu Cys Glu Asn Ser	Val Gln Arg His Ile
20	250	255	260
	Gly His Ala Asn Leu	Thr Phe Glu Gln Leu	Arg Ser Leu Met Glu
	265	270	275
	Ser Leu Pro Gly Lys	Lys Val Gly Ala Glu	Asp Ile Glu Lys Thr
25	280	285	290
	Ile Lys Ala Ser Lys	Pro Ser Asp Gln Ile	Leu Lys Leu Leu Ser
	295	300	305
30	Leu Trp Arg Ile Lys	Asn Gly Asp Gln Asp	Thr Leu Lys Gly Leu
	310	315	320
	Met His Ala Leu Lys	His Ser Lys Thr Tyr	His Phe Pro Lys Thr
	325	330	335
35	Val Thr Gln Ser Leu	Lys Lys Thr Ile Arg	Phe Leu His Ser Phe
	340	345	350
	Thr Met Tyr Lys Leu	Tyr Gln Lys Leu Phe	Leu Glu Met Ile Gly
	355	360	365
40	Asn Gln Val Gln Ser	Val Lys Ile Ser Cys	Leu
	370	375	380

(2) INFORMATION FOR SEQUENCE ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 401

(B) TYPE : amino acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

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(ii) MOLECULE TYPE : Protein (OCIF-C23S)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 66:

5 Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
-20 -15 -10
10 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
-5 -1 1 5
Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
10 15 20
15 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
25 30 35
Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
40 45 50
20 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
55 60 65
Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
70 75 80
25 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
85 90 95
His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
100 105 110
30 Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe
115 120 125
Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
35 130 135 140
Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr
145 150 155
40 His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys
160 165 170
Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala
175 180 185
45 Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp
190 195 200
Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
205 210 215
50 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys
220 225 230

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5 Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile
 235 240 245
 Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile
 250 255 260
 10 Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu
 265 270 275
 Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr
 280 285 290
 15 Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser
 295 300 305
 Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu
 310 315 320
 20 Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr
 325 330 335
 Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe
 340 345 350
 25 Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly
 355 360 365
 Asn Gln Val Gln Ser Val Lys Ile Ser Ser Leu
 30 370 375 380

(2) INFORMATION FOR SEQUENCE ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH : 360
 (B) TYPE : amino acid
 (C) STRANDEDNESS : single
 40 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-DCR1)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 67:

45 Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Pro Cys Pro Asp His Tyr Tyr Thr
 -5 -1 1 5
 50 Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val
 10 15 20
 Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His

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	25	30	35
	Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu		
5	40	45	50
	Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val		
	55	60	65
10	Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro		
	70	75	80
	Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg		
	85	90	95
15	Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys		
	100	105	110
	Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser		
	115	120	125
20	Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe		
	130	135	140
	Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser		
25	145	150	155
	Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser		
	160	165	170
	Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe		
30	175	180	185
	Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile		
	190	195	200
35	Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val		
	205	210	215
	Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg		
	220	225	230
40	Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp		
	235	240	245
	Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu		
45	250	255	260
	Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr		
	265	270	275
	Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His		
50	280	285	290
	Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe		

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295 300 305
 Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu
 310 315 320
 Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
 325 330 335

(2) INFORMATION FOR SEQUENCE ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 359
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-DCR2)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 68:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 -5 -1 1 5
 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 10 15 20
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 25 30 35
 Val Cys Ala Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe
 40 45 50
 Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln
 55 60 65
 Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp
 70 75 80
 Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys
 85 90 95
 His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly
 100 105 110
 Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
 115 120 125
 Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe
 130 135 140

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Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val
 145 150 155
 5 Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val
 160 165 170
 Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln
 175 180 185
 10 Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val
 190 195 200
 Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln
 15 205 210 215
 Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser
 220 225 230
 20 Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile
 235 240 245
 Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys
 250 255 260
 25 Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu
 265 270 275
 Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe
 280 285 290
 30 Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu
 295 300 305
 His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu
 35 310 315 320
 Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
 325 330 335

(2) INFORMATION FOR SEQUENCE ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 363
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF-DCR3)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 69:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser

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	-20		-15		-10	
5	Ile Lys Trp Thr Thr	Gln Glu Thr Phe Pro	Pro Lys Tyr Leu His			
	-5	-1 1	5			
	Tyr Asp Glu Glu Thr	Ser His Gln Leu Leu	Cys Asp Lys Cys Pro			
	10	15	20			
10	Pro Gly Thr Tyr Leu	Lys Gln His Cys Thr	Ala Lys Trp Lys Thr			
	25	30	35			
	Val Cys Ala Pro Cys	Pro Asp His Tyr Tyr	Thr Asp Ser Trp His			
	40	45	50			
15	Thr Ser Asp Glu Cys	Leu Tyr Cys Ser Pro	Val Cys Lys Glu Leu			
	55	60	65			
	Gln Tyr Val Lys Gln	Glu Cys Asn Arg Thr	His Asn Arg Val Cys			
20	70	75	80			
	Arg Cys Pro Asp Gly	Phe Phe Ser Asn Glu	Thr Ser Ser Lys Ala			
	85	90	95			
	Pro Cys Arg Lys His	Thr Asn Cys Ser Val	Phe Gly Leu Leu Leu			
25	100	105	110			
	Thr Gln Lys Gly Asn	Ala Thr His Asp Asn	Ile Cys Ser Gly Asn			
	115	120	125			
30	Ser Glu Ser Thr Gln	Lys Cys Gly Ile Asp	Val Thr Leu Cys Glu			
	130	135	140			
	Glu Ala Phe Phe Arg	Phe Ala Val Pro Thr	Lys Phe Thr Pro Asn			
	145	150	155			
35	Trp Leu Ser Val Leu	Val Asp Asn Leu Pro	Gly Thr Lys Val Asn			
	160	165	170			
	Ala Glu Ser Val Glu	Arg Ile Lys Arg Gln	His Ser Ser Gln Glu			
	175	180	185			
40	Gln Thr Phe Gln Leu	Leu Lys Leu Trp Lys	His Gln Asn Lys Asp			
	190	195	200			
	Gln Asp Ile Val Lys	Lys Ile Ile Gln Asp	Ile Asp Leu Cys Glu			
45	205	210	215			
	Asn Ser Val Gln Arg	His Ile Gly His Ala	Asn Leu Thr Phe Glu			
	220	225	230			
50	Gln Leu Arg Ser Leu	Met Glu Ser Leu Pro	Gly Lys Lys Val Gly			
	235	240	245			
	Ala Glu Asp Ile Glu	Lys Thr Ile Lys Ala	Cys Lys Pro Ser Asp			

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250 255 260
 Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp
 5 265 270 275
 Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys
 280 285 290
 10 Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr
 295 300 305
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys
 310 315 320
 15 Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile
 325 330 335
 Ser Cys Leu
 20 340

(2) INFORMATION FOR SEQUENCE ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH : 359
 (B) TYPE : amino acid
 (C) STRANDEDNESS : single
 30 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF-DCR4)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 70:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 35 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 -5 -1 1 5
 40 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 10 15 20
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 25 30 35
 45 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
 40 45 50
 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
 55 60 65
 50 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
 70 75 80

55

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	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys	
	85	90 95
5	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr	
	100	105 110
	Pro Glu Arg Asn Thr Val Cys Lys Ser Gly Asn Ser Glu Ser Thr	
10	115	120 125
	Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe	
	130	135 140
	Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val	
15	145	150 155
	Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val	
	160	165 170
20	Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln	
	175	180 185
	Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val	
	190	195 200
25	Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln	
	205	210 215
	Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser	
30	220	225 230
	Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile	
	235	240 245
	Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys	
35	250	255 260
	Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu	
	265	270 275
40	Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe	
	280	285 290
	Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu	
	295	300 305
45	His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu	
	310	315 320
	Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu	
50	325	330 335

(2) INFORMATION FOR SEQUENCE ID NO: 71:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 326
 (B) TYPE : amino acid
 (C) STRANDEDNESS : single
 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF-DDD1)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 71:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 -5 -1 1 5
 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 10 15 20
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 25 30 35
 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
 40 45 50
 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
 55 60 65
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
 70 75 80
 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
 85 90 95
 His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
 100 105 110
 Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe
 115 120 125
 Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
 130 135 140
 Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr
 145 150 155
 His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys
 160 165 170
 Gly Ile Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile
 175 180 185
 Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu

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	190	195	200
	Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr		
5	205	210	215
	Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser		
	220	225	230
10	Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu		
	235	240	245
	Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr		
	250	255	260
15	Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe		
	265	270	275
	Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly		
20	280	285	290
	Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu		
	295	300	305

(2) INFORMATION FOR SEQUENCE ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327

(B) TYPE: amino acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF-DDD2)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 72:

	Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser	
	-20	-15 -10
40	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His	
	-5 -1 1 5	
	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro	
	10 15 20	
45	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr	
	25 30 35	
	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His	
50	40 45 50	
	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu	
	55 60 65	

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	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys	
	70	75 80
5	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys	
	85	90 95
	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr	
10	100	105 110
	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe	
	115	120 125
	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn	
15	130	135 140
	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr	
	145	150 155
20	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys	
	160	165 170
	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala	
	175	180 185
25	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp	
	190	195 200
	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile	
	205	210 215
30	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys	
	220	225 230
	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile	
35	235	240 245
	Ile Gln Asp Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys	
	250	255 260
	Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser	
40	265	270 275
	Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile	
	280	285 290
45	Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu	
	295	300 305

(2) INFORMATION FOR SEQUENCE ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 399

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(B) TYPE : amino acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF-CL)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 73:

5
10
15
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Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
-20 -15 -10
Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
-5 -1 1 5
Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
10 15 20
Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
25 30 35
Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
40 45 50
Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
55 60 65
Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
70 75 80
Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
85 90 95
His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
100 105 110
Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe
115 120 125
Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
130 135 140
Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr
145 150 155
His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys
160 165 170
Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala
175 180 185
Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp
190 195 200
Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile

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205	210	215
Lys Arg Gln His Ser	Ser Gln Glu Gln Thr	Phe Gln Leu Leu Lys
220	225	230
Leu Trp Lys His Gln	Asn Lys Asp Gln Asp	Ile Val Lys Lys Ile
235	240	245
Ile Gln Asp Ile Asp	Leu Cys Glu Asn Ser	Val Gln Arg His Ile
250	255	260
Gly His Ala Asn Leu	Thr Phe Glu Gln Leu	Arg Ser Leu Met Glu
265	270	275
Ser Leu Pro Gly Lys	Lys Val Gly Ala Glu	Asp Ile Glu Lys Thr
280	285	290
Ile Lys Ala Cys Lys	Pro Ser Asp Gln Ile	Leu Lys Leu Leu Ser
295	300	305
Leu Trp Arg Ile Lys	Asn Gly Asp Gln Asp	Thr Leu Lys Gly Leu
310	315	320
Met His Ala Leu Lys	His Ser Lys Thr Tyr	His Phe Pro Lys Thr
325	330	335
Val Thr Gln Ser Leu	Lys Lys Thr Ile Arg	Phe Leu His Ser Phe
340	345	350
Thr Met Tyr Lys Leu	Tyr Gln Lys Leu Phe	Leu Glu Met Ile Gly
355	360	365
Asn Gln Val Gln Ser	Val Lys Ile Ser	
370	375	

(2) INFORMATION FOR SEQUENCE ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 351
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : protein (OCIF-CC)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 74:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
-20 -15 -10
Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
-5 -1 1 5

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	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro	
	10	15 20
5	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr	
	25	30 35
	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His	
10	40	45 50
	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu	
	55	60 65
	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys	
15	70	75 80
	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys	
	85	90 95
20	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr	
	100	105 110
	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe	
	115	120 125
25	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn	
	130	135 140
	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr	
	145	150 155
30	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys	
	160	165 170
	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala	
35	175	180 185
	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp	
	190	195 200
	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile	
40	205	210 215
	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys	
	220	225 230
45	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile	
	235	240 245
	Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile	
	250	255 260
50	Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu	
	265	270 275

55

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Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr
 280 285 290
 5 Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser
 295 300 305
 Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu
 10 310 315 320
 Met His Ala Leu Lys His
 325 330

(2) INFORMATION FOR SEQUENCE ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 272
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-CDD2)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 75:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 -5 -1 1 5
 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 10 15 20
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 25 30 35
 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
 40 45 50
 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
 55 60 65
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
 70 75 80
 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
 85 90 95
 His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
 100 105 110
 Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe
 115 120 125

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Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
 130 135 140
 Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr
 145 150 155
 His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys
 160 165 170
 Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala
 175 180 185
 Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp
 190 195 200
 Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 205 210 215
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys
 220 225 230
 Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile
 235 240 245
 Ile Gln
 250

(2) INFORMATION FOR SEQUENCE ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 197

(B) TYPE : amino acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-CDD1)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 76:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 -5 -1 1 5
 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 10 15 20
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 25 30 35
 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His

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40	45	50
Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro	Val Cys Lys Glu Leu	
55	60	65
Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr	His Asn Arg Val Cys	
70	75	80
Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile	Glu Phe Cys Leu Lys	
85	90	95
His Arg Ser Cys Pro Pro Gly Phe Gly Val	Val Gln Ala Gly Thr	
100	105	110
Pro Glu Arg Asn Thr Val Cys Lys Arg Cys	Pro Asp Gly Phe Phe	
115	120	125
Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys	Arg Lys His Thr Asn	
130	135	140
Cys Ser Val Phe Gly Leu Leu Leu Thr Gln	Lys Gly Asn Ala Thr	
145	150	155
His Asp Asn Ile Cys Ser Gly Asn Ser Glu	Ser Thr Gln Lys Cys	
160	165	170
Gly Ile		
175		

(2) INFORMATION FOR SEQUENCE ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 143
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-CCR4)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 77:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser		
-20	-15	-10
Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His		
-5	-1	1
Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro		
10	15	20
Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr		
25	30	35

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Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
 40 45 50
 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
 55 60 65
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
 70 75 80
 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
 85 90 95
 His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
 100 105 110
 Pro Glu Arg Asn Thr Val Cys Lys
 115 120

(2) INFORMATION FOR SEQUENCE ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 106
- (B) TYPE : amino acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-CCR3)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 78:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 -5 -1 1 5
 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 10 15 20
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 25 30 35
 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
 40 45 50
 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
 55 60 65
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
 70 75 80
 Glu

85

(2) INFORMATION FOR SEQUENCE ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 393

(B) TYPE : amino acid

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-CBst)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 79:

```

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
  -20          -15          -10
Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
  -5          -1  1          5
Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
  10          15          20
Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
  25          30          35
Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
  40          45          50
Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
  55          60          65
Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
  70          75          80
Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
  85          90          95
His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
  100         105         110
Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe
  115         120         125
Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
  130         135         140
Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr
  145         150         155
His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys
  160         165         170
Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala

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	175	180	185
5	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp		
	190	195	200
	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile		
	205	210	215
10	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys		
	220	225	230
	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile		
	235	240	245
15	Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile		
	250	255	260
	Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu		
20	265	270	275
	Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr		
	280	285	290
	Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser		
25	295	300	305
	Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu		
	310	315	320
30	Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr		
	325	330	335
	Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe		
	340	345	350
35	Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly		
	355	360	365
	Asn Leu Val		
40	370		

(2) INFORMATION FOR SEQUENCE ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

45	(A) LENGTH : 321
	(B) TYPE : amino acid
	(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-CSph)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 80:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser

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	-20		-15		-10
	Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His				
5	-5		-1 1		5
	Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro				
	10		15		20
10	Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr				
	25		30		35
	Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His				
	40		45		50
15	Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu				
	55		60		65
	Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys				
20	70		75		80
	Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys				
	85		90		95
	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr				
25	100		105		110
	Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe				
	115		120		125
30	Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn				
	130		135		140
	Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr				
	145		150		155
35	His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys				
	160		165		170
	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala				
40	175		180		185
	Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp				
	190		195		200
	Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile				
45	205		210		215
	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys				
	220		225		230
50	Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile				
	235		240		245
	Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile				

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250 255 260
 Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu
 265 270 275
 Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr
 280 285 290
 Ile Lys Ala Ser Leu Asp
 295 300

(2) INFORMATION FOR SEQUENCE ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 292
- (B) TYPE : amino acid
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-CBsp)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 81:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 -5 -1 1 5
 10 15 20
 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 25 30 35
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 40 45 50
 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
 55 60 65
 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
 70 75 80
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
 85 90 95
 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
 100 105 110
 His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
 115 120 125
 Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe
 130 135 140

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Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
 145 150 155
 Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr
 160 165 170
 His Asp Asn Ile Cys Ser Gly
 175 180

(2) INFORMATION FOR SEQUENCE ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 84
- (B) TYPE : amino acid
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : Protein (OCIF-CPst)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 82:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
 -20 -15 -10
 Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
 -5 -1 1 5
 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
 10 15 20
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
 25 30 35
 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
 40 45 50
 Thr Ser Asp Glu Cys Leu Tyr Leu Val
 55 60 63

(2) INFORMATION FOR SEQUENCE ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 1206
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-C19S)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 83:

5 ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 10 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA 420
 GTTTGCAAAA GATGTCCAGA TGGGTTCCTC TCAAATGAGA CGTCATCTAA AGCACCCTGT 480
 AGAAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 15 CACGACAACA TATGTTCCGG AACAGTGAA TCAACTCAAA AAAGTGAAT AGATGTTACC 600
 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 20 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA 960
 25 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020
 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAACT 1080
 GTCATCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG 1140
 30 TATCAGAACT TATTTTGTAG AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC 1200
 TTATAA 1206

(2) INFORMATION FOR SEQUENCE ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 1206

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-C20S)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 84:

45 ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 50 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300

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CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA 420
 5 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480
 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600
 10 CTGAGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 AAAAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAAACAGC 840
 15 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA 960
 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAATGG CGACCAAGAC 1020
 20 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAACT 1080
 GTCCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTACA GCTTCACAAT GTACAAATTG 1140
 TATCAGAAAGT TATTTTGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC 1200
 TTATAA 1206

(2) INFORMATION FOR SEQUENCE ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 1206

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-C21S)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 85:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 45 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA 420
 50 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480
 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600

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CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 5 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCAG TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 10 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA 960
 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAATGG CGACCAAGAC 1020
 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAACT 1080
 GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG 1140
 15 TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC 1200
 TTATAA 1206

(2) INFORMATION FOR SEQUENCE ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 1206

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-C22S)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 86:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 35 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 40 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA 420
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAAATGAGA CGTCATCTAA AGCACCTGT 480
 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 45 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC 600
 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 50 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900

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AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCAAGCAAA 960
 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020
 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAACT 1080
 GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG 1140
 TATCAGAAAGT TATTTTGTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC 1200
 TTATAA 1206

(2) INFORMATION FOR SEQUENCE ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 1206
- (B) TYPE : nucleic acid
- (C) STRANDEDNESS : single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-C23S)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 87:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGTACCTTG AGATAGAGTT CTGCTTAAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA 420
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480
 AGAAAAACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600
 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA 960
 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020
 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAACT 1080
 GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG 1140
 TATCAGAAAGT TATTTTGTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCAGC 1200

TTATAA

1206

(2) INFORMATION FOR SEQUENCE ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 1083

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-DCR1)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 88:

ATGAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAACCTT	GCCCTGACCA	CTACTACACA	GACAGCTGGC	ACACCAGTGA	CGAGTGTCTA	120
TACTGCAGCC	CCGTGTGCAA	GGAGCTGCAG	TACGTCAAGC	AGGAGTGCAA	TCGCACCCAC	180
AACCGCGTGT	GCGAATGCAA	GGAAGGGCGC	TACCTTGAGA	TAGAGTTCTG	CTTGAAACAT	240
AGGAGCTGCC	CTCCTGGATT	TGGAGTGGTG	CAAGCTGGAA	CCCCAGAGCG	AAATACAGTT	300
TGCAAAAGAT	GTCCAGATGG	GTTCTTCTCA	AATGAGACGT	CATCTAAAGC	ACCCTGTAGA	360
AAACACACAA	ATTGCAGTGT	CTTTGGTCTC	CTGCTAATCT	AGAAAGGAAA	TGCAACACAC	420
GACAACATAT	GTTCCGGAAA	CAGTGAATCA	ACTCAAAAAT	GTGGAATAGA	TGTTACCCTG	480
TGTGAGGAGG	CATTCTTCAG	GTTTGCTGTT	CCTACAAAGT	TTACGCCTAA	CTGGCTTAGT	540
GTCTTGGTAG	ACAATTTGCC	TGGCACCAAA	GTAACGCAG	AGAGTGTAGA	GAGGATAAAA	600
CGGCAACACA	GCTCACAGA	ACAGACTTTC	CAGCTGCTGA	AGTTATGGAA	ACATCAAAAC	660
AAAGACCAAG	ATATAGTCAA	GAAGATCATC	CAAGATATTG	ACCTCTGTGA	AAACAGCGTG	720
CAGCGGCACA	TTGGACATGC	TAACCTCACC	TTCGAGCAGC	TTCGTAGCTT	GATGGAAAGC	780
TTACCGGGAA	AGAAAGTGGG	AGCAGAAGAC	ATTGAAAAAA	CAATAAAGGC	ATGCAAACCC	840
AGTGACCAGA	TCCTGAAGCT	GCTCAGTTTG	TGGCGAATAA	AAAATGGCGA	CCAAGACACC	900
TTGAAGGGCC	TAATGCACGC	ACTAAAGCAC	TCAAAGACGT	ACCACTTTCC	CAAAACTGTC	960
ACTCAGAGTC	TAAAGAAGAC	CATCAGGTTT	CTTCACAGCT	TCACAAATGTA	CAAATTGTAT	1020
CAGAAGTTAT	TTTTAGAAAT	GATAGGTAAC	CAGGTCCAAT	CAGTAAAAAT	AAGCTGCTTA	1080
TAA						1083

(2) INFORMATION FOR SEQUENCE ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 1080

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

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(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-DCR2)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 89:

ATGAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
GTGTGCGCCC AATGCAAGGA AGGGCGCTAC CTTGAGATAG AGTTCTGCTT GAAACATAGG 240
AGCTGCCCTC CTGGATTGAG AGTGGTGCAA GCTGGAACCC CAGAGCGAAA TACAGTTTGC 300
AAAAGATGTC CAGATGGGTT CTCTCAAAT GAGACGTCAT CTAAAGCACC CTGTAGAAAA 360
CACACAAATT GCAGTGCTTT TGGTCTCCTG CTAATCAGA AAGGAAATGC AACACACGAC 420
AACATATGTT CCGGAAACAG TGAATCAACT CAAAAATGTG GAATAGATGT TACCCTGTGT 480
GAGGAGGCAT TCTTCAGGTT TGCTGTTTCT ACAAAGTTTA CGCCTAACTG GCTTAGTGTC 540
TTGGTAGACA ATTTGCCTGG CACCAAAGTA AACGCAGAGA GTGTAGAGAG GATAAAACGG 600
CAACACAGCT CACAAGAACA GACTTTCCAG CTGCTGAAGT TATGGAAACA TCAAAACAAA 660
GACCAAGATA TAGTCAAGAA GATCATCCAA GATATTGACC TCTGTGAAAA CAGCGTGCAG 720
CGGCACATTG GACATGCTAA CCTCACCTTC GAGCAGCTTC GTAGCTTGAT GGAAAGCTTA 780
CCGGGAAAGA AAGTGGGAGC AGAAGACATT GAAAAACAA TAAAGGCATG CAAACCCAGT 840
GACCAGATCC TGAAGCTGCT CAGTTTGTGG CGAATAAAAA ATGGCGACCA AGACACCTTG 900
AAGGGCCTAA TGCACGCACT AAAGCACTCA AAGACGTACC ACTTTCCCAA AACTGTCACT 960
CAGAGTCTAA AGAAGACCAT CAGGTTCCCT CACAGCTTCA CAATGTACAA ATTGTATCAG 1020
AAGTTATTTT TAGAAATGAT AGGTAACCAG GTCCAATCAG TAAAAATAAG CTGCTTATAA 1080

(2) INFORMATION FOR SEQUENCE ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 1092

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-DCR3)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 90:

ATGAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240

CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCAGATG TCCAGATGGG TTCTTCTCAA ATGAGACGTC ATCTAAAGCA 360
 CCCTGTAGAA AACACACAAA TTGCAGTGTC TTTGGTCTCC TGCTAACTCA GAAAGGAAAT 420
 GCAACACACG ACAACATATG TTCCGGAAAC AGTGAATCAA CTCAAAAATG TGAATAGAT 480
 GTTACCCTGT GTGAGGAGGC ATTCTTCAGG TTTGCTGTTC CTACAAAGTT TACGCCTAAC 540
 TGGCTTAGTG TCTTGGTAGA CAATTTGCCT GGCACCAAAG TAAACGCAGA GAGTGTAGAG 600
 AGGATAAAAC GGCAACACAG CTCACAAGAA CAGACTTTCC AGCTGCTGAA GTTATGGAAA 660
 CATCAAAACA AAGACCAAGA TATAGTCAAG AAGATCATCC AAGATATTGA CCTCTGTGAA 720
 AACAGCGTGC AGCGGCACAT TGGACATGCT AACCTCACCT TCGAGCAGCT TCGTAGCTTG 780
 ATGGAAAGCT TACCGGGAAA GAAAGTGGGA GCAGAAGACA TTGAAAAAAC AATAAAGGCA 840
 TGCAAACCCA GTGACCAGAT CCTGAAGCTG CTCAGTTTGT GGCGAATAAA AAATGGCGAC 900
 CAAGACACCT TGAAGGGCCT AATGCACGCA CTAAGCACT CAAAGACGTA CCACTTTCCC 960
 AAAACTGTCA CTCAGAGTCT AAAGAAGACC ATCAGGTTCC TTCACAGCTT CACAATGTAC 1020
 AAATTGTATC AGAAGTTATT TTTAGAAATG ATAGGTAACC AGGTCCAATC AGTAAAAATA 1080
 AGCTGCTTAT AA 1092

(2) INFORMATION FOR SEQUENCE ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 1080

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-DCR4)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 91:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA 420
 GTTTGCAAAT CCGGAAACAG TGAATCAACT CAAAAATGTG GAATAGATGT TACCCTGTGT 480
 GAGGAGGCAT TCTTCAGGTT TGCTGTTCCT ACAAAGTTTA CGCCTAACTG GCTTAGTGTC 540
 TTGGTAGACA ATTTGCCTGG CACCAAGTA AACGCAGAGA GTGTAGAGAG GATAAACCGG 600
 CAACACAGCT CACAAGAACA GACTTTCAG CTGCTGAAGT TATGGAAACA TCAAAACAAA 660

5 GACCAAGATA TAGTCAAGAA GATCATCCAA GATATTGACC TCTGTGAAAA CAGCGTGCAG 720
 CGGCACATTG GACATGCTAA CCTCACCTTC GAGCAGCTTC GTAGCTTGAT GGAAAGCTTA 780
 CCGGGAAAGA AAGTGGGAGC AGAAGACATT GAAAAACAA TAAAGGCATG CAAACCCAGT 840
 GACCAGATCC TGAAGCTGCT CAGTTTGTGG CGAATAAAAA ATGGCGACCA AGACACCTTG 900
 AAGGGCCTAA TGCACGCACT AAAGCACTCA AAGACGTACC ACTTTCCCAA AACTGTCAC 960
 10 CAGAGTCTAA AGAAGACCAT CAGGTTCCCT CACAGCTTCA CAATGTACAA ATTGTATCAG 1020
 AAGTTATTTT TAGAAATGAT AGGTAACCAG GTCCAATCAG TAAAAATAAG CTGCTTATAA 1080

(2) INFORMATION FOR SEQUENCE ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 981

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-DDD1)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 92:

25 ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTG 120
 30 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 35 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA 420
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480
 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATATTGAC 600
 40 CTCTGTGAAA ACAGCGTGCA GCGGCACATT GGACATGCTA ACCTCACCTT CGAGCAGCTT 660
 CGTAGCTTGA TGGAAAGCTT ACCGGGAAAG AAAGTGGGAG CAGAAGACAT TGAAAAACA 720
 ATAAAGGCAT GCAAACCCAG TGACCAGATC CTGAAGCTGC TCAGTTTGTG GCGAATAAAA 780
 45 AATGGCGACC AAGACACCTT GAAGGGCCTA ATGCACGCAC TAAAGCACTC AAAGACGTAC 840
 CACTTTCCCA AACTGTGAC TCAGAGTCTA AAGAAGACCA TCAGGTTCTT TCACAGCTTC 900
 ACAATGTACA AATTGTATCA GAAGTTATTT TTAGAAATGA TAGGTAACCA GGTCCAATCA 960
 50 GTAAAAATAA GCTGCTTATA A 981

(2) INFORMATION FOR SEQUENCE ID NO: 93:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 984

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-DDD2)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 93:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA 420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT 480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGACG CACTAAAGCA CTCAAAGACG 840
TACCACTTTC CAAAACTGT CACTCAGAGT CTAAGAAGA CCATCAGGTT CCTTCACAGC 900
TTCACAATGT ACAAATTGTA TCAGAAGTTA TTTTAGAAA TGATAGGTAA CCAGGTCCAA 960
TCAGTAAAAA TAAGCTGCTT .ATAA 984

(2) INFORMATION FOR SEQUENCE ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 1200

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CL)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 94:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60

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CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA 420
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480
 AGAAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600
 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAACACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA 960
 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020
 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAACT 1080
 GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG 1140
 TATCAGAAGT TATTTTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTAA 1200

(2) INFORMATION FOR SEQUENCE ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 1056

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CC)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 95:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA 420

GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480
 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 5 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600
 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 10 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA 960
 15 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020
 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTGA 1056

(2) INFORMATION FOR SEQUENCE ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 819

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CDD2)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 96:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 35 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGCA GCGAAATACA 420
 40 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480
 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600
 45 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660
 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 50 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAATGA 819

(2) INFORMATION FOR SEQUENCE ID NO: 97:

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(2) INFORMATION FOR SEQUENCE ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 321

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CCR3)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 99:

ATGAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
CACAACCGCG TGTGCGAATG A 321

(2) INFORMATION FOR SEQUENCE ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 1182

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CBst)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 100:

ATGAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA 420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
CAGGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660

AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 5 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA 960
 10 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020
 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT 1080
 GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG 1140
 TATCAGAAGT TATTTT TAGA AATGATAGGT AACCTAGTCT AG 1182

(2) INFORMATION FOR SEQUENCE ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 966

(B) TYPE : nucleic acid

(C) STRANDEDNESS : single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CSph)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 101:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
 30 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 35 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA 420
 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480
 40 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600
 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCTTACAA AGTTTACGCC TAACTGGCTT 660
 45 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720
 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780
 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840
 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900
 50 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCTAGTCTA 960
 GACTAG 966

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 594
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CDD1)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 97:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA 420
GTTTGCAAAA GATGTCCAGA TGGGTCTTTC TCAAATGAGA CGTCATCTAA AGCACCTGT 480
AGAAAACACA CAAATTGCAG TGTCTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT ATGA. 594

(2) INFORMATION FOR SEQUENCE ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 432
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CCR4)

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 98:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA 420
GTTTGCAAAAT GA 432

(2) INFORMATION FOR SEQUENCE ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 564
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-CBsp)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 102:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA 420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCTGT 480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540
CACGACAACA TATGTTCCGG CTAG 564

(2) INFORMATION FOR SEQUENCE ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH : 255
(B) TYPE : nucleic acid
(C) STRANDEDNESS : single
(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : cDNA (OCIF-Pst)

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 103:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
CTATACCTAG TCTAG 255

(2) INFORMATION FOR SEQUENCE ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH : 1317

(B) TYPE : nucleic acid

(C) STRANDEDNESS : double

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : human OCIF genomic DNA-1

(xi) SEQUENCE DESCRIPTION :SEQ ID NO: 104:

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15 CTGGAGACAT ATAACTTGAA CACTTGGCCC TGATGGGGAA GCAGCTCTGC AGGGACTTTT 60
   TCAGCCATCT GTAAACAATT TCAGTGGCAA CCCGCGAACT GTAATCCATG AATGGGACCA 120
   CACTTTACAA GTCATCAAGT CTAATTCTA GACCAGGGAA TTAATGGGGG AGACAGCGAA 180
20 CCCTAGAGCA AAGTGCCAAA CTTCTGTCGA TAGCTTGAGG CTAGTGGAAA GACCTCGAGG 240
   AGGCTACTCC AGAAGTTCAG CGCGTAGGAA GCTCCGATAC CAATAGCCCT TTGATGATGG 300
   TGGGGTTGGT GAAGGGAACA GTGCTCCGCA AGGTTATCCC TGCCCCAGGC AGTCCAATTT 360
   TCACTCTGCA GATTCTCTCT GGCTCTAACT ACCCCAGATA ACAAGGAGTG AATGCAGAAT 420
25 AGCACGGGCT TTAGGGCCAA TCAGACATTA GTTAGAAAAA TTCCTACTAC ATGGTTTATG 480
   TAAACTTGAA GATGAATGAT TGCGAACTCC CCGAAAAGGG CTCAGACAAT GCCATGCATA 540
   AAGAGGGGCC CTGTAATTTG AGGTTTCAGA ACCCGAAGTG AAGGGGTCAG GCAGCCGGGT 600
30 ACGGCGGAAA CTCACAGCTT TCGCCAGCG AGAGGACAAA GGTCTGGGAC AACTCCAAC 660
   TCGCTCCGGA TCTTGGCTGG ATCGGACTCT CAGGGTGGAG GAGACACAAG CACAGCAGCT 720
   GCCCAGCGTG TGCCAGCCC TCCCACCGCT GGTCCCGGCT GCCAGGAGGC TGGCCGCTGG 780
   CGGGAAGGGG CCGGGAACC TCAGAGCCCC GCGGAGACAG CAGCCGCCTT GTTCTCAGC 840
35 CCGGTGGCTT TTTTTCGCC TGCTTCCCA GGGACAGAC ACCACGCCC CACCCTCAC 900
   GCCCCACCTC CCTGGGGGAT CCTTTCGCC CCAGCCCTGA AAGCGTTAAT CCTGGAGCTT 960
   TCTGCACACC CCCCAGCCG TCCGCCCCA GCTTCCTAAA AAAGAAAGGT GCAAAGTTTG 1020
40 GTCCAGGATA GAAAAATGAC TGATCAAAGG CAGGCGATAC TTCCTGTTGC CGGGACGCTA 1080
   TATATAACGT GATGAGCGCA CGGGCTGCGG AGACGCACCG GAGCGCTCGC CCAGCCGCCG 1140
   CCTCCAAGCC CCTGAGGTTT CCGGGGACCA CA ATG AAC AAG TTG CTG TGC TGC 1193

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Met Asn Lys Leu Leu Cys Cys

-20

-15

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GCG CTC GTG GTAAGTCCCT GGGCCAGCCG ACGGGTGCCC GGCGCCTGGG 1242
Ala Leu Val

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GAGGCTGCTG CCACCTGGTC TCCCAACCTC CCAGCGGACC GGCGGGGAAA AAGGCTCCAC 1302

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TCGCTCCCTC CCAAG

1317

5 (2) INFORMATION FOR SEQUENCE ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH :

10 (B) TYPE : nucleic acid

(C) STRANDEDNESS : double

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE : human OCIF genomic DNA-2

15 (xi) SEQUENCE DESCRIPTION :SEQ ID NO: 105:

GCTTACTTTG TGCCAAATCT CATTAGGCTT AAGGTAATAC AGGACTTTGA GTCAAATGAT @60
 20 ACTGTTGCAC ATAAGAACAA ACCTATTTTC ATGCTAAGAT GATGCCACTG TGTTCCTTTC 120
 TCCTTCTAG TTT CTG GAC ATC TCC ATT AAG TGG ACC ACC CAG GAA ACG TTT 171
 Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr Phe
 -10 -5 -1 1

25 CCT CCA AAG TAC CTT CAT TAT GAC GAA GAA ACC TCT CAT CAG CTG TTG 219
 Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu Leu
 5 10 15

30 TGT GAC AAA TGT CCT CCT GGT ACC TAC CTA AAA CAA CAC TGT ACA GCA 267
 Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala
 20 25 30 35

35 AAG TGG AAG ACC GTG TGC GCC CCT TGC CCT GAC CAC TAC TAC ACA GAC 315
 Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp
 40 40 45 50

45 AGC TGG CAC ACC AGT GAC GAG TGT CTA TAC TGC AGC CCC GTG TGC AAG 363
 Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys
 55 60 65

50 GAG CTG CAG TAC GTC AAG CAG GAG TGC AAT CGC ACC CAC AAC CGC GTG 411
 Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val
 70 75 80

55

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	TGC GAA TGC AAG GAA GGG CGC TAC CTT GAG ATA GAG TTC TGC TTG AAA	459
	Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys	
5	85 90 95	
	CAT AGG AGC TGC CCT CCT GGA TTT GGA GTG GTG CAA GCT G GTACGTGTCA	509
10	His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala	
	100 105 110	
	ATGTGCAGCA AAATTAATTA GGATCATGCA AAGTCAGATA GTTGTGACAG TTAGGAGAA	569
15	CACTTTTGTT CTGATGACAT TATAGGATAG CAAATTGCAA AGGTAATGAA ACCTGCCAGG	629
	TAGGTACTAT GTGTCTGGAG TGCTTCCAAA GGACCATTGC TCAGAGGAAT ACTTTGCCAC	689
	TACAGGGCAA TTTAATGACA AATCTCAAAT GCAGCAAATT ATTCTCTCAT GAGATGCATG	749
20	ATGGTTTTTT TTTTTTTTTT TAAAGAAACA AACTCAAGTT GCACTATTGA TAGTTGATCT	809
	ATACCTCTAT ATTTCACTTC AGCATGGACA CCTTCAAACCT GCAGCACTTT TTGACAAACA	869
	TCAGAAATGT TAATTTATAC CAAGAGAGTA ATTATGCTCA TATTAATGAG ACTCTGGAGT	929
	GCTAACAATA AGCAGTTATA ATTAATTATG TAAAAAATGA GAATGGTGAG GGAATTGCA	989
25	TTTCATTATT AAAACAAGG CTAGTTCTTC CTTTAGCATG GGAGCTGAGT GTTTGGGAGG	1049
	GTAAGGACTA TAGCAGAATC TCTTCAATGA GCTTATTCTT TATCTTAGAC AAAACAGATT	1109
	GTCAAGCCAA GAGCAAGCAC TTGCCTATAA ACCAAGTGCT TTCTCTTTTG CATTTTGAAC	1169
30	AGCATTGGTC AGGGCTCATG TGTATTGAAT CTTTAAACC AGTAACCCAC GTTTTTTTTC	1229
	TGCCACATTT GCGAAGCTTC AGTGCAGCCT ATAACTTTTC ATAGCTTGAG AAAATTAAGA	1289
	GTATCCACTT ACTTAGATGG AAGAAGTAAT CAGTATAGAT TCTGATGACT CAGTTTGAAG	1349
	CAGTGTCTCT CAACTGAAGC CCGCTGATA TTTTAAGAAA TATCTGGATT CCTAGGCTGG	1409
35	ACTCCTTTTT GTGGGCAGCT GTCCTGCGCA TTGTAGAATT TTGGCAGCAC CCCTGGACTC	1469
	TAGCCACTAG ATACCAATAG CAGTCCTTCC CCCATGTGAC AGCCAAAAAT GTCTTCAGAC	1529
	ACTGTCAAAT GTCGCCAGGT GGCAAAATCA CTCCTGGTTG AGAACAGGGT CATCAATGCT	1589
40	AAGTATCTGT AACTATTITTA ACTCTCAAAA CTTGTGATAT ACAAAGTCTA AATTATTAGA	1649
	CGACCAATAC TTTAGGTTTA AAGGCATACA AATGAAACAT TCAAAAATCA AAATCTATTC	1709
	TGTTTCTCAA ATAGTGAATC TTATAAAATT AATCACAGAA GATGCAAATT GCATCAGAGT	1769
	CCCTTAAAT TCCTCTTCGT ATGAGTATTT GAGGGAGGAA TTGGTGATAG TTCCTACTTT	1829
45	CTATTGGATG GTACTTTGAG ACTCAAAAGC TAAGCTAAGT TGTGTGTGTG TCAGGGTGCG	1889
	GGGTGTGGAA TCCCATCAGA TAAAAGCAAA TCCATGIAAT TCATTGAGTA AGTTGTATAT	1949
	GTAGAAAAAT GAAAAGTGGG CTATGCAGCT TGGAAACTAG AGAATTTTGA AAAATAATGG	2009
50	AAATCACAAG GATCTTTCTT AAATAAGTAA GAAAATCTGT TTGTAGAATG AAGCAAGCAG	2069
	GCAGCCAGAA GACTCAGAAC AAAAGTACAC ATTTTACTCT GTGTACACTG GCAGCAGAGT	2129
	GGGATTTATT TACCTCTCCC TCCCTAAAAA CCCACACAGC GGTTCCTCTT GGGAAATAAG	2189

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	AGGTTTCCAG CCCAAAGAGA AGGAAAGACT ATGTGGTGTT ACTCTAAAAA GTATTTAATA	2249
	ACCGTTTTGT TGTGCTGTT GCTGTTTTGA AATCAGATTG TCTCCTCTCC ATATTTTATT	2309
5	TACTTCATTG TGTTAATTCC TGTGGAATTA CTTAGAGCAA GCATGGTGAA TTCTCAACTG	2369
	TAAAGCCAAA TTTCTCCATC ATTATAATTT CACATTTTGC CTGGCAGGTT ATAATTTTAA	2429
	TATTTCCACT GATAGTAATA AGGTAAAAATC AITACTTAGA TGGATAGATC TTTTTCATAA	2489
10	AAAGTACCAT CAGTTATAGA GGAAGTCAT GTTCATGTTT AGGAAGGTCA TTAGATAAAG	2549
	CTTCTGAATA TATTATGAAA CATTAGTTCT GTCATTCTTA GATTCTTTTT GTTAAATAAC	2609
	TTTAAAAGCT AACTTACCTA AAAGAAATAT CTGACACATA TGAACCTCTC ATTAGGATGC	2669
	AGGAGAAGAC CCAAGCCACA GATATGTATC TGAAGAATGA ACAAGATTCT TAGGCCCGGC	2729
15	ACGGTGGCTC ACATCTGTAA TCTCAAGAGT TTGAGAGGTC AAGGCGGGCA GATCACCTGA	2789
	GGTCAGGAGT TCAAGACCAG CCTGGCCAAC ATGATGAAAC CCTGCCTCTA CTAAAAATAC	2849
	AAAAATTAGC AGGGCATGGT GGTGCATGCC TGCAACCCTA GCTACTCAGG AGGCTGAGAC	2909
20	AGGAGAATCT CTTGAACCCT CGAGGCGGAG GTTGTGGTGA GCTGAGATCC CTCTACTGCA	2969
	CTCCAGCCTG GGTGACAGAG ATGAGACTCC GTCCCTGCCG CCGCCCCCGC CTCCCCCCCC	3029
	AAAAAGATTC TTCTTCATGC AGAACATACG GCAGTCAACA AAGGGAGACC TGGGTCCAGG	3089
	TGTCCAAGTC ACTTATTTTC AGTAAATTAG CAATGAAAGA ATGCCATGGA ATCCCTGCCC	3149
25	AAATACCTCT GCTTATGATA TTGTAGAATT TGATATAGAG TTGTATCCCA TTAAAGGAGT	3209
	AGGATGTAGT AGGAAAGTAC TAAAAACAAA CACACAAACA GAAAAACCTC TTTGCTTTGT	3269
	AAGGTGGTTC CTAAGATAAT GTCAGTGCAA TGCTGGAAAT AATATTTAAT ATGTGAAGGT	3329
30	TTTAGGCTGT GTTTTCCCTT CCTGTTCTTT TTTTCTGCCA GCCCTTTGTC ATTTTTCAG	3389
	GTCAATGAAT CATGTAGAAA GAGACAGGAG ATGAAACTAG AACCAGTCCA TTTTGCCCTT	3449
	TTTTTTATTT TCTGGTTTTG GTAAAAGATA CAATGAGGTA GGAGGTTGAG ATTTATAAAT	3509
	GAAGTTTAAAT AAGTTTCTGT AGCTTTGATT TTTCTCTTTC ATATTTGTTA TCTTGATAA	3569
35	GCCAGAATTG GCCTGTAAAA TCTACATATG GATATTGAAG TCTAAATCTG TTCAACTAGC	3629
	TTCACTAGA TGGAGATATT TTCATATTCA GATACACTGG AATGTATGAT CTAGCCATGC	3689
	GTAATATAGT CAAGTGTTTG AAGGTATTTA TTTTAAATAG CGTCTTTAGT TGTGGACTGG	3749
40	TTCAAGTTTT TCTGCCAATG ATTTCTTCAA ATTTATCAAA TATTTTCCA TCATGAAGTA	3809
	AAATGCCCTT GCAGTCACCC TTCCTGAAGT TTGAACGACT CTGCTGTTTT AAACAGTTTA	3869
	AGCAAATGGT ATATCATCTT CCGTTTACTA TGTAGCTTAA CTGCAGGCTT ACGCTTTTGA	3929
	GTCAGCGGCC AACTTTATTG CCACCTTCAA AAGTTTATTA TAATGTTGTA AATTTTACT	3989
45	TCTCAAGGTT AGCATACTTA GGAGTTGCTT CACAATTAGG ATTCAGGAAA GAAAGAACTT	4049
	CAGTAGGAAC TGATTGGAAT TTAATGATGC AGCATTCAAT GGGTACTAAT TTCAAAGAAT	4109
	GATATTACAG CAGACACACA GCAGTTATCT TGATTTTCTA GGAATAATTG TATGAAGAAT	4169
50	ATGGCTGACA ACACGGCCTT ACTGCCACTC AGCGGAGGCT GGACTAATGA ACACCCTACC	4229
	CTTCTTTCCT TTCCTCTCAC ATTTTCATGAG CGTTTGTAG GTAACGAGAA AATTGACTTG	4289
	CATTTGCATT ACAAGGAGGA GAACTGGCA AAGGGGATGA TGGTGGAAGT TTTGTTCTGT	4349

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	CTAATGAAGT GAAAAATGAA AATGCTAGAG TTTTGTGCAA CATAATAGTA GCAGTAAAAA	4409
	CCAAGTGAAA AGTCTTTCCA AAACGTGTGT AAGAGGGCAT CTGCTGGGAA ACGATTGAG	4469
5	GAGAAGGTAC TAAATTGCTT GGTATTTTCC GTAG GA ACC CCA GAG CGA AAT ACA	4523
	Gly Thr Pro Glu Arg Asn Thr	
	115	
10	GTT TGC AAA AGA TGT CCA GAT GGG TTC TTC TCA AAT GAG ACG TCA TCT	4571
	Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser	
	120 125 130 135	
15	AAA GCA CCC TGT AGA AAA CAC ACA AAT TGC AGT GTC TTT GGT CTC CTG	4619
	Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu	
	140 145 150	
20	CTA ACT CAG AAA GGA AAT GCA ACA CAC GAC AAC ATA TGT TCC GGA AAC	4667
	Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn	
25	155 160 165	
	AGT GAA TCA ACT CAA AAA TGT GGA ATA G GTAATTACAT TCCAAAATAC	4715
30	Ser Glu Ser Thr Gln Lys Cys Gly Ile	
	170 175	
35	GTCTTTGTAC GATTTTGTAG TATCATCTCT CTCTCTGAGT TGAACACAAG GCCTCCAGCC	4775
	ACATTCTTGG TCAAACTTAC ATTTTCCCTT TCTTGAATCT TAACCAGCTA AGGCTACTCT	4835
	CGATGCATTA CTGCTAAAGC TACCACTCAG AATCTCTCAA AAACATCATCT TCTCACAGAT	4895
	AACACCTCAA AGCTTGATT TCTCTCCTTT CACACTGAAA TCAAATCTTG CCCATAGGCA	4955
40	AAGGGCAGTG TCAAGTTTGC CACTGAGATG AAATTAGGAG AGTCCAAACT GTAGAATTCA	5015
	CGTTGTGTGT TATTACTTTC ACGAATGTCT GTATTATTAA CTAAAGTATA TATTGGCAAC	5075
	TAAGAAGCAA AGTGATATAA ACATGATGAC AAATTAGGCC AGGCATGGTG GCTTACTCCT	5135
	ATAATCCCAA CATTTTGGGG GGCCAAGGTA GGCAGATCAC TTGAGGTCAG GATTTCAGA	5195
45	CCAGCCTGAC CAACATGGTG AAACCTTGTC TCTACTAAAA ATACAAAAAT TAGCTGGGCA	5255
	TGGTAGCAGG CACTTCTAGT ACCAGCTACT CAGGGCTGAG GCAGGAGAAT CGCTTGAACC	5315
	CAGGAGATGG AGGTTGCAGT GAGCTGAGAT TGTACCACTG CACTCCAGTC TGGGCAACAG	5375
	AGCAAGATTT CATCACACAC ACACACACAC ACACACACAC ACACATTAGA AATGTGTACT	5435
50	TGGCTTTGTT ACCTATGGTA TTAGTGCATC TATTGCATGG AACTTCCAAG CTA CTCTGTGT	5495
	TGTGTTAAGC TCTTCATTGG GTACAGGTCA CTAGTATTAA GTTCAGGTTA TTCGGATGCA	5555

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	TTCCACGGTA GTGATGACAA TTCATCAGGC TAGTGTGTGT GTTCACCTTG TCACTCCAC	5615
	CACTAGACTA ATCTCAGACC TTCACTCAA GACACATTAC ACTAAAGATG ATTTGCTTTT	5675
5	TTGTGTTTAA TCAAGCAATG GTATAAACCA GCTTGACTCT CCCCAAACAG TTTTTCGTAC	5735
	TACAAAGAAG TTTATGAAGC AGAGAAATGT GAATTGATAT ATATATGAGA TTCTAACCCA	5795
	GTTCCAGCAT TGTTTCATTG TGTAATTGAA ATCATAGACA AGCCATTTTA GCCTTTGCTT	5855
10	TCTTATCTAA AAAAAAAAAA AAAAAAATGA AGGAAGGGGT ATTAAGGA GTGATCAAAT	5915
	TTTAACATTG TCTTTAATTA ATTCAATTTT AATTTTACTT TTTTTCATTT ATTGTGCACT	5975
	TACTATGTGG TACTGTGCTA TAGAGGCTTT AACATTTATA AAAACACTGT GAAAGTTGCT	6035
	TCAGATGAAT ATAGGTAGTA GAACGGCAGA ACTAGTATTC AAAGCCAGGT CTGATGAATC	6095
15	CAAAAACAAA CACCCATTAC TCCCATTTTC TGGGACATAC TTA CTCTACC CAGATGCTCT	6155
	GGGCTTTGTA ATGCCTATGT AAATAACATA GTTTTATGTT TGGTTATTTT CCTATGTAAT	6215
	GTCTACTTAT ATATCTGTAT CTATCTCTTG CTTTGTTC AAAGGTAAAC TATGTGTCTA	6275
20	AATGTGGGCA AAAAATAACA CACTATTCCA AATTACTGTT CAAATTCCTT TAAGTCAGTG	6335
	ATAATTATTT GTTTTGACAT TAATCATGAA GTTCCCTGTG GGTACTAGGT AAACCTTTAA	6395
	TAGAATGTTA ATGTTTGAT TCATTATAAG AATTTTGGC TGTTACTTAT TTACAACAAT	6455
	ATTTCACTCT AATTAGACAT TACTAACT TTCTCTGAA AACAAATGCC AAAAAGAAC	6515
25	ATTAGAAGAC ACGTAAGCTC AGTTGGTCTC TGCCACTAAG ACCAGCCAAC AGAAGCTTGA	6575
	TTTTATTCAA ACTTTGCATT TTAGCATATT TTATCTGGA AAATTCAATT GTGTTGGTTT	6635
	TTTGTTTTGG TTTGTATTGA ATAGACTCTC AGAAATCCAA TTGTTGAGTA AATCTTCTGG	6695
30	GTTCCTAAC CTTTCTTTAG AT GTT ACC CTG TGT GAG GAG GCA TTC TTC AGG	6747
	Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg	
	180 185	
35	TTT GCT GTT CCT ACA AAG TTT ACG CCT AAC TGG CTT AGT GTC TTG GTA	6795
	Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val	
	190 195 200	
40	GAC AAT TTG CCT GGC ACC AAA GTA AAC GCA GAG AGT GTA GAG AGG ATA	6843
	Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile	
	205 210 215	
45	AAA CGG CAA CAC AGC TCA CAA GAA CAG ACT TTC CAG CTG CTG AAG TTA	6891
	Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu	
50	220 225 230 235	
	TGG AAA CAT CAA AAC AAA GAC CAA GAT ATA GTC AAG AAG ATC ATC CAA G	6940

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Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln

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GTAATTACAT	TCCAAAATAC	GTCTTTGTAC	GATTTTGTAG	TATCATCTCT	CTCTCTGAGT	7000
TGAACACAAG	GCCTCCAGCC	ACATTCTTGG	TCAAACCTTAC	ATTTTCCCTT	TCTTGAATCT	7060
TAACCAGCTA	AGGCTACTCT	CGATGCATTA	CTGCTAAAGC	TACCACTCAG	AATCTCTCAA	7120
AAACTCATCT	TCTCACAGAT	AACACCTCAA	AGCTTGATT	TCTCTCCTTT	CACACTGAAA	7180
TCAAATCTTG	CCCATAGGCA	AAGGGCAGTG	TCAAGTTTGC	CACTGAGATG	AAATTAGGAG	7240
AGTCCAAACT	GTAGAATTCA	CGTTGTGTGT	TATTACTTTC	ACGAATGTCT	GTATTATTAA	7300
CTAAAGTATA	TATTGGCAAC	TAAGAAGCAA	AGTGATATAA	ACATGATGAC	AAATTAGGCC	7360
AGGCATGGTG	GCTTACTCCT	ATAATCCCAA	CATTTTGGGG	GGCCAAGGTA	GGCAGATCAC	7420
TTGAGGTCAG	GATTTCAAGA	CCAGCCTGAC	CAACATGGTG	AAACCTTGTC	TCTACTAAAA	7480
ATACAAAAAT	TAGCTGGGCA	TGGTAGCAGG	CACTTCTAGT	ACCAGCTACT	CAGGGCTGAG	7540
GCAGGAGAAT	CGCTTGAACC	CAGGAGATGG	AGGTTCAGT	GAGCTGAGAT	TGTACCACTG	7600
CACTCCAGTC	TGGGCAACAG	AGCAAGATTT	CATCACACAC	ACACACACAC	ACACACACAC	7660
ACACATTAGA	AATGTGTACT	TGGCTTTGTT	ACCTATGGTA	TTAGTGCATC	TATTGCATGG	7720
AACTTCCAAG	CTACTCTGGT	TGTGTTAAGC	TCTTCATTGG	GTACAGGTCA	CTAGTATTAA	7780
GTTCAGGTTA	TTCGGATGCA	TTCCACGGTA	GTGATGACAA	TTCATCAGGC	TAGTGTGTGT	7840
GTTACCTTG	TCACTCCAC	CACTAGACTA	ATCTCAGACC	TCACTCAAA	GACACATTAC	7900
ACTAAAGATG	ATTTGCTTTT	TTGTGTTTAA	TCAAGCAATG	GTATAAACCA	GCTTGACTCT	7960
CCCCAAACAG	TTTTTCGTAC	TACAAAGAAG	TTTATGAAGC	AGAGAAATGT	GAATTGATAT	8020
ATATATGAGA	TTCTAACCCA	GTTCCAGCAT	TGTTTCATTG	TGTAATTGAA	ATCATAGACA	8080
AGCCATTTTA	GCCTTTGCTT	TCTTATCTAA	AAAAAAAAAA	AAAAAAATGA	AGGAAGGGGT	8140
ATTAAAAGGA	GTGATCAAAT	TTTAACATT	TCTTTAATTA	ATTCATTTT	AATTTTACTT	8200
TTTTTCATTT	ATTGTGCACT	TACTATGTGG	TACTGTGCTA	TAGAGGCTTT	AACATTTATA	8260
AAAACACTGT	GAAAGTTGCT	TCAGATGAAT	ATAGGTAGTA	GAACGGCAGA	ACTAGTATTC	8320
AAAGCCAGGT	CTGATGAATC	CAAAAACAAA	CACCCATTAC	TCCCATTTTC	TGGGACATAC	8380
TTACTCTACC	CAGATGCTCT	GGGCTTTGTA	ATGCCTATGT	AAATAACATA	GTTTTATGTT	8440
TGGTTATTTT	CCTATGTAAT	GTCTACTTAT	ATATCTGTAT	CTATCTCTTG	CTTTGTTTCC	8500
AAAGGTAAAC	TATGTGTCTA	AATGTGGGCA	AAAAATAACA	CACTATTCCA	AATTACTGTT	8560
CAAATTCCTT	TAAGTCAGTG	ATAATTATTT	GTTTTGACAT	TAATCATGAA	GTTCCCTGTG	8620
GGTACTAGGT	AAACCTTTAA	TAGAATGTTA	ATGTTTGTAT	TCATTATAAG	AATTTTGGC	8680
TGTTACTTAT	TTACAACAAT	ATTTCACTCT	AATTAGACAT	TTACTAACT	TTCTCTTGAA	8740
AACAATGCCC	AAAAAAGAAC	ATTAGAAGAC	ACGTAAGCTC	AGTTGGTCTC	TGCCACTAAG	8800
ACCAGCCAAC	AGAAGCTTGA	TTTTATTCAA	ACITTCGATT	TTAGCATATT	TTATCTTGGA	8860
AAATTCAATT	GTGTTGGTTT	TTTGTTTTTG	TTTGTTATTGA	ATAGACTCTC	AGAAATCCAA	8920

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	TTGTTGAGTA AATCTTCTGG GTTTTCTAAC CTTTCTTTAG AT ATT GAC CTC TGT	8974
5	Asp Ile Asp Leu Cys 255	
10	GAA AAC AGC GTG CAG CGG CAC ATT GGA CAT GCT AAC CTC ACC TTC GAG Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu 260 265 270	9022
15	CAG CTT CGT AGC TTG ATG GAA AGC TTA CCG GGA AAG AAA GTG GGA GCA Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala 275 280 285	9070
20	GAA GAC ATT GAA AAA ACA ATA AAG GCA TGC AAA CCC AGT GAC CAG ATC Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile 290 295 300	9118
25	CTG AAG CTG CTC AGT TTG TGG CGA ATA AAA AAT GGC GAC CAA GAC ACC Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr 305 310 315 320	9166
30	TTG AAG GGC CTA ATG CAC GCA CTA AAG CAC TCA AAG ACG TAC CAC TTT Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe 325 330 335	9214
35	CCC AAA ACT GTC ACT CAG AGT CTA AAG AAG ACC ATC AGG TTC CTT CAC Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His 340 345 350	9262
40	AGC TTC ACA ATG TAC AAA TTG TAT CAG AAG TTA TTT TTA GAA ATG ATA Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile 355 360 365	9310
45	GGT AAC CAG GTC CAA TCA GTA AAA ATA AGC TGC TTA TAACTGGAAA Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu 370 375 380	9356

5 TGGCCATTGA GCTGTTTCCT CACAATTGGC GAGATCCCAT GGATGAGTAA ACTGTTTCTC 9416
 AGGCACTTGA GGCTTTTCACT GATATCTTTC TCATTACCAG TGAATAATTT TGCCACAGGG 9476
 TACTAAAAGA AACTATGATG TGGAGAAAGG ACTAACATCT CCTCCAATAA ACCCCAAATG 9536
 GTTAATCCAA CTGTCAGATC TGGATCGTTA TCTACTGACT ATATTTTCCC TTATTACTGC 9596
 TTGCAGTAAT TCAACTGGAA ATTAACAAAA AAAAATACTAGA CTCCACTGGG CCTTACTAAA 9656
 10 TATGGGAATG TCTAACTTAA ATAGCTTTGG GATTCCAGCT ATGCTAGAGG CTTTATTAG 9716
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 GGAGTATTT TATAATTTA TCTGTATAAG CTGTAATATC ATTTTATAGA AAATGCATTA 10016
 TTTAGTCAAT TGTTTAATGT TGGAAACAT ATGAAATATA AATTATCTGA ATATTAGATG 10076
 20 CTCTGAGAAA TTGAATGTAC CTTATTTAAA AGATTTTATG GTTTTATAAC TATATAAATG 10136
 ACATTATTAA AGTTTTCAAA TTATTTTAA TTGCTTCTC TGTTGCTTTT ATTT 10190

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Claims

30 1. A protein characterized by the following properties:

(a) molecular weights on SDS-polyacrylamide gel electrophoresis (SDS-PAGE)

35 ; approximately 60 kD under reducing conditions
 ; approximately 60 kD and 120 kD under non-reducing conditions

(b) a high affinity to cation-exchange column and heparin column

(c) a biological activity to inhibit osteoclast differentiation and/or maturation

40 ; its activity is decreased by heating at 70°C for 10 min or at 56°C for 30 min.
 ; its activity is lost by heating at 90 °C for 10 min

(d) internal amino acid sequences provided in sequence numbers 1, 2, and 3.

45 2. A protein of claim 1 having N-terminal amino acid sequences provided in sequence number 7.

3. A protein of claim 1 produced in human fibroblasts.

50 4. A method of producing the protein of claim 1, 2, and 3 by the following process: cultivating human fibroblasts ; purifying the protein by a combination of ion-exchange column, affinity-column and reverse phase-column chromatography.

5. A method of producing the protein of claim 4 by cultivating human fibroblasts on alumina ceramic pieces.

55 6. A protein with amino acid sequence provided in sequence number 4.

7. cDNAs encoding amino acid sequence provided in sequence number 4.

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8. cDNA with nucleotide sequence provided in sequence number 6.
9. cDNAs that hybridize to cDNA provided in sequence number 6 under moderately stringent conditions.
- 5 10. A protein expressed from cDNA encoding amino acid sequence provided in sequence number 4.
11. A protein with a biological activity to inhibit osteoclast differentiation and/or maturation, that obtain as amino acid expressed cDNA sharing at least 80 % sequence identity with the amino acid sequence provided in sequence number 4.
- 10 12. A method of production of the protein with the following properties and inhibit osteoclast differentiation and/or maturation by gene engineering using cDNA encoding amino acid sequence provided in sequence number 4:
- (a) molecular weights on SDS-polyacrylamide gel electrophoresis (SDS-PAGE)
- 15 ; approximately 60 kD under reducing conditions
; approximately 60 kD and 120 kD under non-reducing conditions
- (b) a high affinity to cation-exchange column and heparin column
- 20 (c) ; inhibit osteoclast differentiation and/or maturation activity is decreased by heating at 70°C for 10 min or at 56°C for 30 min
; its activity is lost by heating at 90 °C for 10 min
- 25 (d) internal amino acid sequence provided in sequence number 1-3.
13. A method of producing the protein according to claim 10 by gene engineering using mammalian cells as host cells.
14. A method of producing the protein according to claim 13 by gene engineering using 293/EBNA cells or CHO cells as mammalian host cells.
- 30 15. A cDNA with nucleotide sequence provided in sequence number 8.
16. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 8.
- 35 17. cDNAs encoding amino acid sequence provided in sequence number 9.
18. A cDNA with nucleotide sequence provided in sequence number 10.
- 40 19. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 10.
20. cDNAs encoding amino acid sequence provided in sequence number 11.
21. A cDNA with nucleotide sequence provided in sequence number 12.
- 45 22. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 12.
23. cDNAs encoding amino acid sequence provided in sequence number 13.
- 50 24. A cDNA with nucleotide sequence provided in sequence number 14.
25. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 14.
26. cDNAs encoding amino acid sequence provided in sequence number 15.
- 55 27. A cDNA with nucleotide sequence provided in sequence number 83.
28. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 83.

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29. cDNAs encoding amino acid sequence provided in sequence number 62.
30. A cDNA with nucleotide sequence provided in sequence number 84.
- 5 31. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 84.
32. cDNAs encoding amino acid sequence provided in sequence number 63.
33. A cDNA with nucleotide sequence provided in sequence number 85.
- 10 34. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 85.
35. cDNAs encoding amino acid sequence provided in sequence number 64.
- 15 36. A cDNA with nucleotide sequence provided in sequence number 86.
37. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 86.
38. cDNAs encoding amino acid sequence provided in sequence number 65.
- 20 39. A cDNA with nucleotide sequence provided in sequence number 87.
40. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 87.
- 25 41. cDNAs encoding amino acid sequence provided in sequence number 66.
42. A cDNA with nucleotide sequence provided in sequence number 88.
43. A protein encoded by a cDNA having a sequence provided in sequence number 88.
- 30 44. cDNAs encoding amino acid sequence provided in sequence number 67.
45. A cDNA with nucleotide sequence provided in sequence number 89.
- 35 46. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 89.
47. cDNAs encoding amino acid sequence provided in sequence number 68.
48. A cDNA with nucleotide sequence provided in sequence number 90.
- 40 49. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 90.
50. cDNAs encoding amino acid sequence provided in sequence number 69.
- 45 51. A cDNA with nucleotide sequence provided in sequence number 91.
52. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 91.
53. cDNAs encoding amino acid sequence provided in sequence number 70.
- 50 54. A cDNA with nucleotide sequence provided in sequence number 92.
55. A protein encoded by a cDNA having a nucleotide sequence provided in number 92.
- 55 56. cDNAs encoding amino acid sequence provided in sequence number 71.
57. A cDNA with nucleotide sequence provided in sequence number 93.

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58. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 93.
59. cDNAs encoding amino acid sequence provided in sequence number 72.
- 5 60. A cDNA with nucleotide sequence provided in sequence number 94.
61. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 94.
62. cDNAs encoding amino acid sequence provided in sequence number 73.
- 10 63. A cDNA with nucleotide sequence provided in sequence number 95.
64. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 95.
- 15 65. cDNAs encoding amino acid sequence provided in sequence number 74.
66. A cDNA with nucleotide sequence provided in sequence number 96.
67. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 96.
- 20 68. cDNAs encoding amino acid sequence provided in sequence number 75.
69. A cDNA with nucleotide sequence provided in sequence number 97.
- 25 70. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 97.
71. cDNAs encoding amino acid sequence provided in sequence number 76.
72. A cDNA with nucleotide sequence provided in sequence number 98.
- 30 73. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 98.
74. cDNAs encoding amino acid sequence provided in sequence number 77.
- 35 75. A cDNA with nucleotide sequence provided in sequence number 99.
76. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 99.
77. cDNAs encoding amino acid sequence provided in sequence number 78.
- 40 78. A cDNA with nucleotide sequence provided in sequence number 100.
79. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 100.
- 45 80. cDNAs encoding amino acid sequence provided in sequence number 79.
81. A cDNA with nucleotide sequence provided in sequence number 101.
82. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 101.
- 50 83. cDNAs encoding amino acid sequence provided in sequence number 80.
84. A cDNA with nucleotide sequence provided in sequence number 102.
- 55 85. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 102.
86. cDNAs encoding amino acid sequence provided in sequence number 81.

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87. A cDNA with nucleotide sequence provided in sequence number 103.

88. A protein encoded by a cDNA having a nucleotide sequence provided in sequence number 103.

5 89. cDNAs encoding amino acid sequence provided in sequence number 82.

90. Genomic DNAs encoding the amino acid sequence provided in sequence number 4.

10 91. Genomic DNAs of Claim 90 with the nucleotide sequence provided in sequence number 104 or 105.

92. An antibody having specific affinity to the OCIF

93. An antibody of Claim 92 that is polyclonal antibody.

15 94. An antibody of Claim 92 that is monoclonal antibody.

95. A monoclonal antibody of Claim 94 being characterized by the following properties.
Molecular weight of about 150,000, and of subclass IgG₁, IgG_{2a}, or IgG_{2b}.

20 96. A method of determining the concentration of the protein of the OCIF using the antibodies of Claim 92, 93, 94, and 95.

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Fig. 1

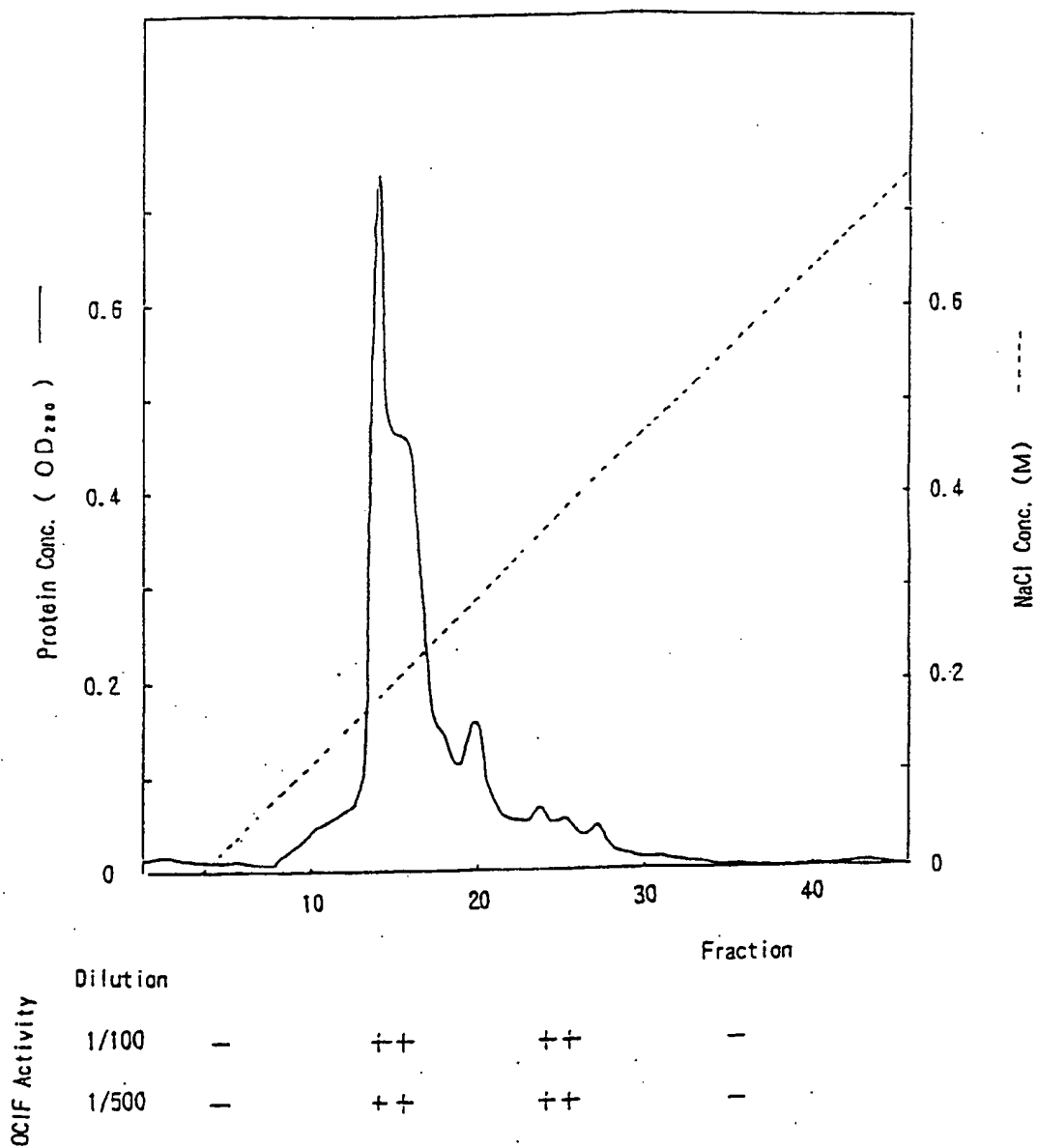


Fig. 2

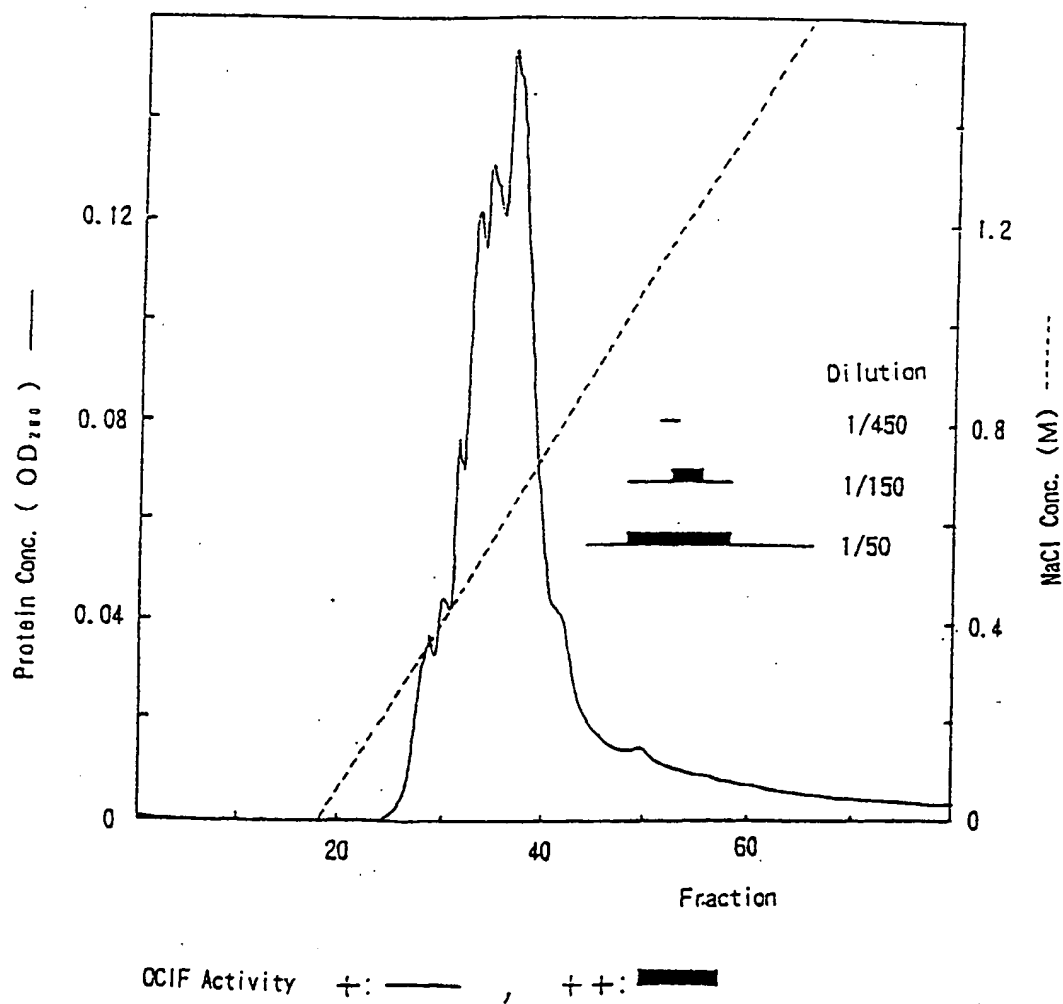


Fig. 3

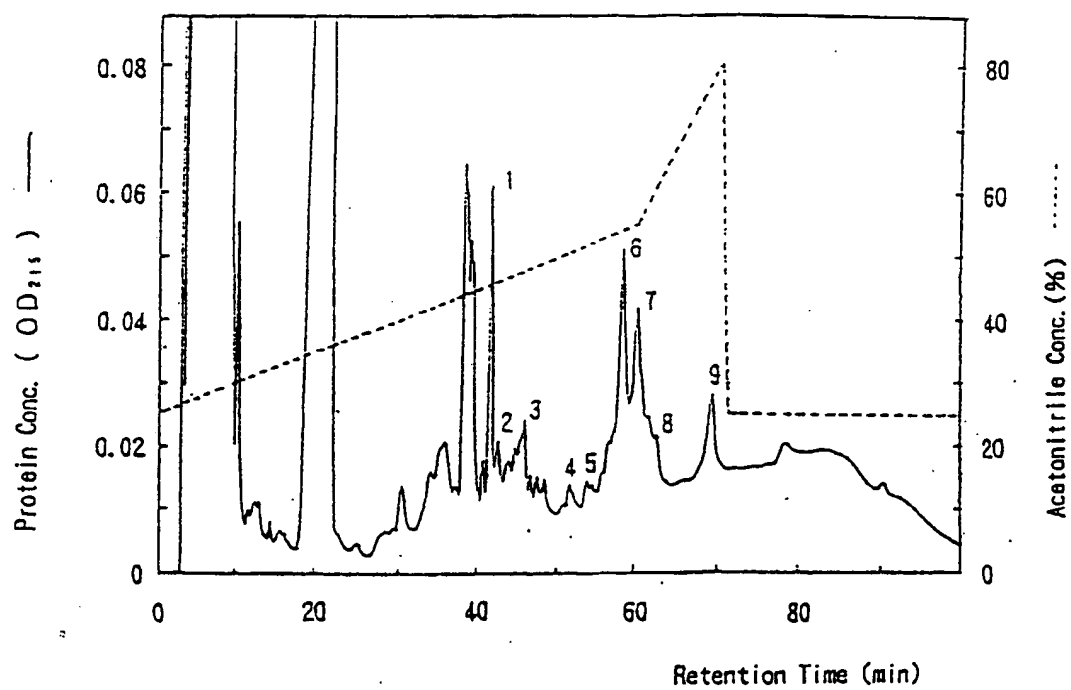


Fig. 4

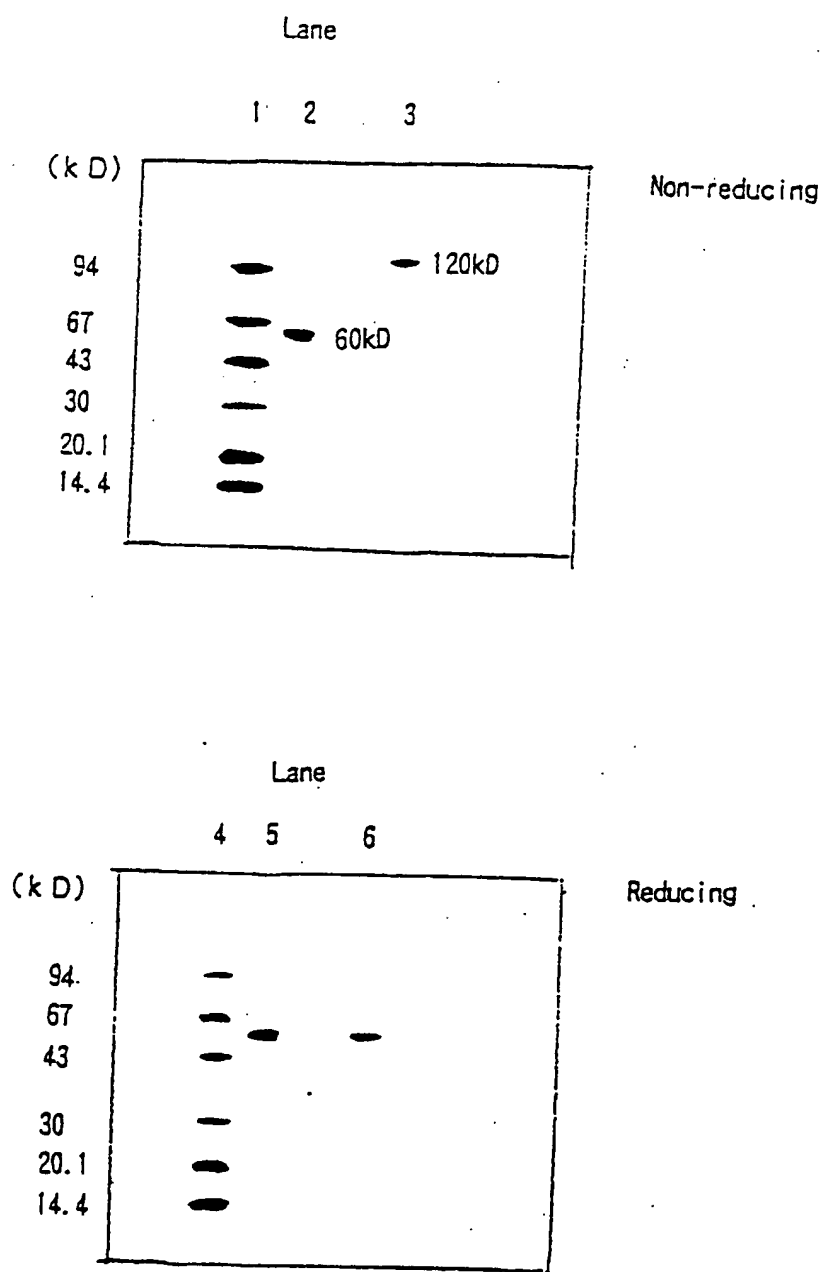


Fig.5

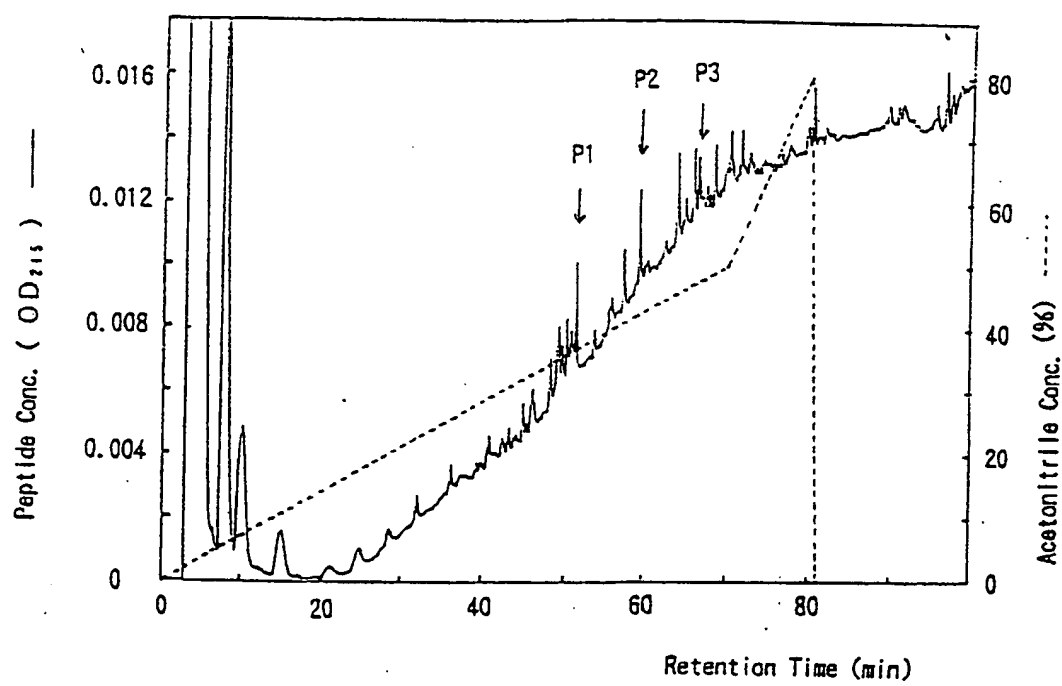


Fig. 6

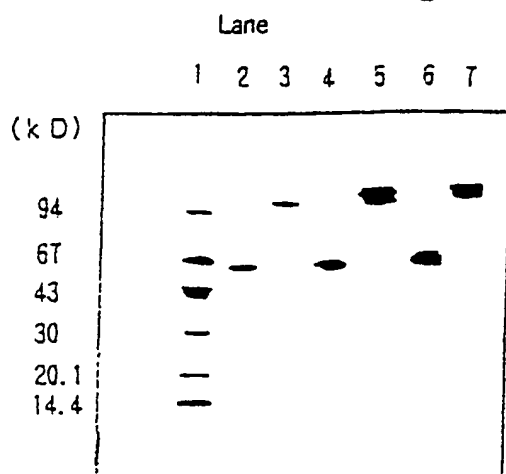


Fig. 7

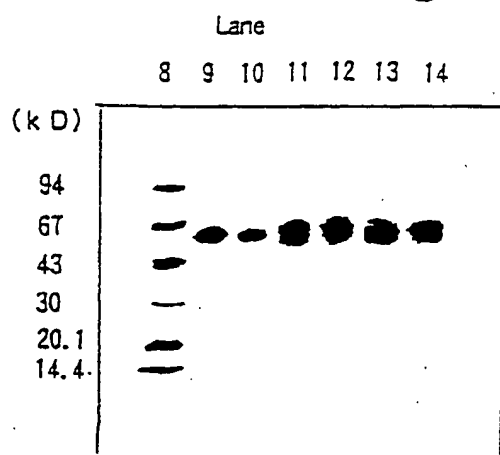


Fig. 8

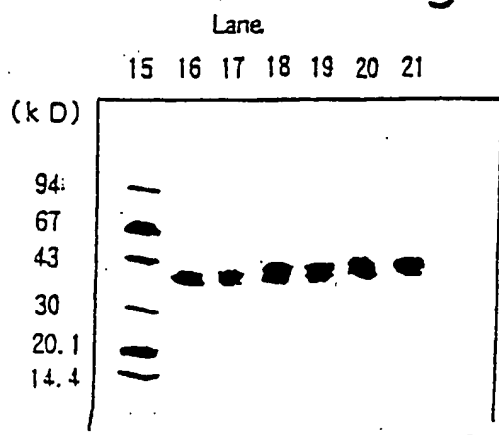


Fig. 9

1
MNNLLCCALVFLDISIKWTTQETFPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKT (OCIF1)

MNNLLCCALVFLDISIKWTTQETFPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKT (OCIF2)
1

61
VCAPCPDHYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLK (OCIF1)

VCAPCPDHYTDSWHTSDECLYCSPVCKE-----CNRTHNRVCECKEGRYLEIEFCLK (OCIF2)
61

121
HRSCPPGFGVVQAGTPERN TVCKRCPDGGFSNETSSKAPCRKHTNCSVFGLLLTQKGNAT (OCIF1)

HRSCPPGFGVVQAGTPERN TVCKRCPDGGFSNETSSKAPCRKHTNCSVFGLLLTQKGNAT (OCIF2)
114

181
HDNICS GNSESTQKCGIDVTLCEEAFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERI (OCIF1)

HDNICS GNSESTQKCGIDVTLCEEAFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERI (OCIF2)
174

241
KRQHSSQEQT FQLKLWKHQNKDQDIVKKIIQDIDLCE NSVQRHIGHANLT FEQLRSLME (OCIF1)

KRQHSSQEQT FQLKLWKHQNKDQDIVKKIIQDIDLCE NSVQRHIGHANLT FEQLRSLME (OCIF2)
234

301
SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRIKNGDQDTLKGLMHALKH SKTYHFPKT (OCIF1)

SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRIKNGDQDTLKGLMHALKH SKTYHFPKT (OCIF2)
294

361
VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL (OCIF1)

VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL (OCIF2)
354

Fig. 10

```

1
MNNLLCCALVFLOISIKWTTQETFPKYLHYDEETSHQLLCKCPCPGTYLKQHCTAKWKT (OCIF1)
** *****
MNNLLCCALVFLOISIKWTTQETFPKYLHYDEETSHQLLCKCPCPGTYLKQHCTAKWKT (OCIF3)
1

61
VCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLK (OCIF1)
*****
VCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLK (OCIF3)
61

121
HRSCPPGFGVVQAGTPERN TVCKRCPDGGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNAT (OCIF1)
*****
HRSCPPGFGVVQAGTPERN TVCKRCPDGGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNAT (OCIF3)
121

181
HDNICS GNSESTQKCGIDVTLCEEAFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERI (OCIF1)
*****
HDNICS GNSESTQKCGIDVTLCEEAFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERI (OCIF3)
181

241
KRQHSSQEQTFLLLKWKHQNKDQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLME (OCIF1)
*****
KRQHSSQEQTFLLLKWKHQNKDQDIVKKIIQDIDLCENSVQRHIGHANLS----- (OCIF3)
241

301
SLPGKKVGAEDIEKTIKACKPSDQILKLLSLWRIKNGDQDTLKGLMHALKHSKTYHFPKT (OCIF1)
*****
-----LWRIKNGDQDTLKGLMHALKHSKTYHFPKT (OCIF3)
292

361
VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL (OCIF1)
*****
VTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL (OCIF3)
322

```

Fig. 11

1
MNNLLCCALVFLDISIKWTTQETFPKYLHYDEETSHQLLCKCPPGTYLKQHCTAKWKT (OCIF1)
** *****
MNNLLCCSLVFLDISIKWTTQETFPKYLHYDEETSHQLLCKCPPGTYLKQHCTAKWKT (OCIF4)
1
61
VCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLK (OCIF1)

VCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLK (OCIF4)
61
121
HRSCPPGFGVVQAGTPERNTVCKRCPDGGFSNETSSKAPCRKHTNCSVFGLLLTQKGNAT (OCIF1)

HRSCPPGFGVVQAGTCQCAAKLIRIMQSQIVVTV (OCIF4)
121

Fig. 12

1
MNNLLCCALVFLDISIKWTTQETFPKYLHYDEETSHQLLCKCPPGTYLKQHCTAKWKT (OCIF1)
** *****
MNNLLCCALVFLDISIKWTTQETFPKYLHYDEETSHQLLCKCPPGTYLKQHCTAKWKT (OCIF5)
1
61
VCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLK (OCIF1)

VCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLK (OCIF5)
61
121
HRSCPPGFGVVQAGTPERNTVCKRCPDGGFSNETSSKAPCRKHTNCSVFGLLLTQKGNAT (OCIF1)
***** *
HRSCPPGFGVVQAGCRRRPKPQICI (OCIF5)
121

Fig. 13

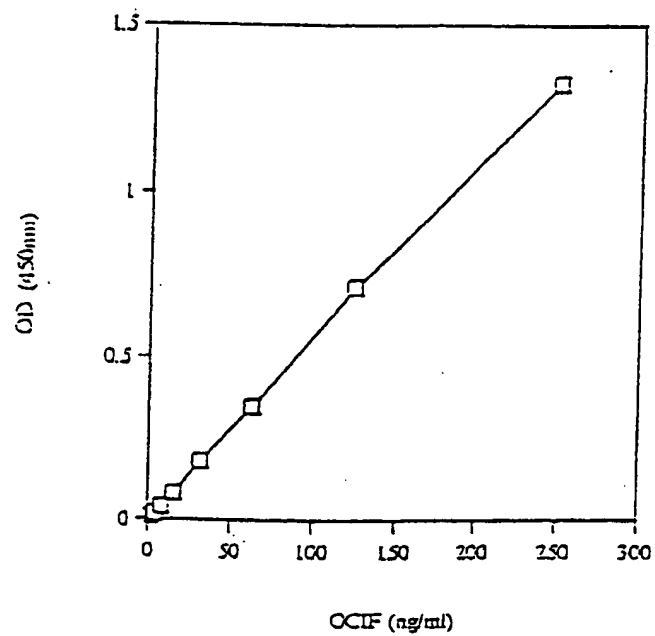


Fig. 14

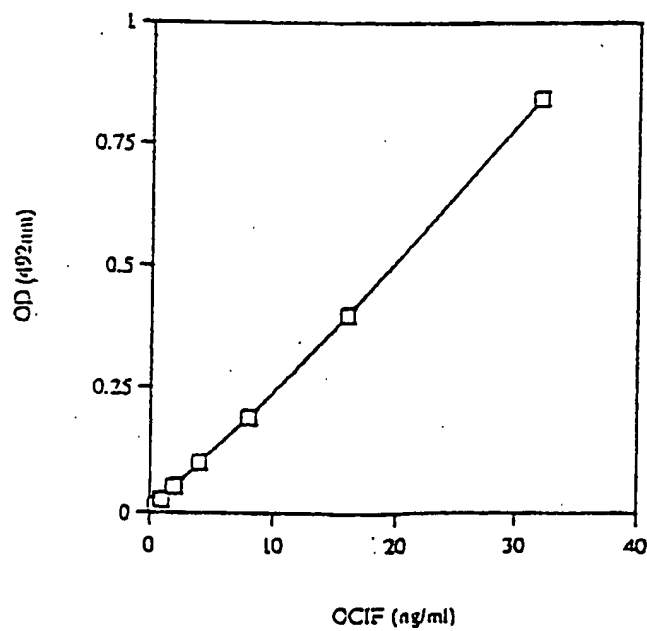
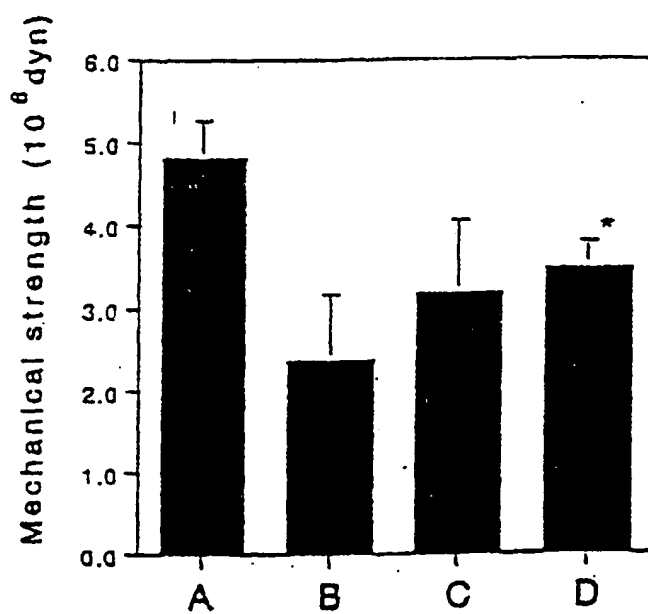


Fig. 15



A : Normal rat

B : Denervated rat + Vehicle

C : Denervated rat + OCIF 10 μ g/kg/day

D : Denervated rat + OCIF 100 μ g/kg/day

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP96/00374

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl⁶ C07K14/52, C07K16/24, C12N15/19, C12N15/06, C12N5/08,
C12N5/10, C12N5/20, C12P21/02, C12P21/08, G01N33/577

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int. Cl⁶ C07K14/52, C07K16/24, C12N15/19, C12N15/06, C12N5/08,
C12N5/10, C12N5/20, C12P21/02, C12P21/08, G01N33/577

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

BIOSIS PREVIEWS, CAS ONLINE, WPI, WPI/L

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Fawthrop, F.W. et al. "The effect of transforming growth factor beta on the plasminogen activator activity of normal human osteoblast-like cells and a human osteosarcoma cell line MG-63", J. Bone. Miner. Res. (1992) Vol. 7, No. 12, p. 1363-1371	1 - 96
A	Fenton, A.J. et al. "Long-term culture of disaggregated rat osteoclasts inhibition of bone resorption and reduction of osteoclast-like cell number by calcitonin and PTHrP107-139", J. Cell Physiol. (1993) Vol. 155, No. 1, p. 1-7	1 - 96

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

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Date of the actual completion of the international search

May 14, 1996 (14. 05. 96)

Date of mailing of the international search report

May 28, 1996 (28. 05. 96)

Name and mailing address of the ISA/

Japanese Patent Office

Facsimile No.

Authorized officer

Telephone No.

binant plasmid containing the 5.8 kb EcoRI/NotI fragment was isolated and this plasmid was termed pBSG8-5.8. pBSG8-5.8 was digested with HindIII and 0.9 kb of DNA fragment derived from this digestion was isolated in the same manner as described above. This 0.9 kb fragment was then cloned in pBluescript II SK- at the HindIII site as described above. This recombinant plasmid containing 0.9 kb HindIII fragment was denoted pBS8H0.9.

5 λOIF11 DNA was digested with EcoRI and 6 kb, 3.6 kb, 2.6 kb EcoRI fragments were isolated in the same manner as described above and cloned in pBluescript II SK+ vector at the EcoRI site as described above. These recombinant plasmids were termed pBSG11-6, pBSG11-3.6, and pBSG11-2.6, respectively. pBSG11-6 was digested with HindIII and the digest was applied on a 0.7 % agarose gel. Three fragments, 2.2 kb, 1.1 kb, and 1.05 kb in length, were extracted from the gel and cloned independently in pBluescript II SK- vector at the HindIII site in the same manner as described above. These recombinant plasmids were termed pBS6H2.2, pBS6H1.1 and pBS6H1.05, respectively.

10 The nucleotide sequence of the cloned genomic DNA was determined using ABI Dye-deoxy Terminator Cycle Sequencing Ready Reaction Kit (PERKIN ELMER) and 373A DNA Sequencing system (Applied Biosystems). Plasmids pBSG8-5.8, pBS8H0.9, pBSG11-6, pBSG11-3.6, pBSG11-2.6, pBS6H2.2, pBS6H1.1 and pBS6H1.05 were prepared according to the alkaline-SDS procedure as described in Molecular Cloning: A Laboratory Manual and used as templates for the DNA sequence analysis. Nucleotide sequence of the human OCIF gene was presented in Sequence No 104 and Sequence No 105. The nucleotide sequence of the DNA, between exon 1 and exon 2 was not entirely determined. There is a stretch of approximately 17 kb of nucleotides between the sequences given in sequence No. 104 and sequence No. 105.

20 EXAMPLE 24

Quantitation of OCIF by EIA

i) Preparation of anti-OCIF antibody

25 Male JW rabbits (Kitayama LABES Co., LTD) weighing 2.5-3.0 kg were used for immunization for preparing antisera. Three male JW rabbits (Kitayama LABES Co., LTD) weighing 2.5-3.0 kg were used for immunization. For immunization, emulsion was prepared by mixing an equal volume of rOCIF (200 µg/ml) and complete Freund's adjuvant (Difco, Cat. 0638-60-7). The rabbits were immunized subcutaneously six times at the interval of one week with 1 ml of emulsion per injection. The rabbits were injected six times at the interval of seven days subcutaneously. Whole blood was obtained ten days after the final immunization and serum was separated. Antibody was purified from serum as follows. Antiserum was diluted two-fold with PBS. After adding ammonium sulfate at a final concentration of 40 w/v %, antiserum was allowed to stand at 4 °C for 1 hr.. Precipitate obtained by centrifugation at 8000 x g for 20 min. was dissolved in a small volume of PBS and was dialyzed against PBS. The resulting solution was loaded onto a Protein G-Sepharose column (Pharmacia). After washing with PBS, absorbed immunoglobulin G was eluted with 0.1 M glycine-HCL buffer (pH 3.0). Elutes were neutralized with 1.5 M Tris-HCL buffer (pH 8.7) immediately and were dialyzed against PBS. Protein concentration was determined by absorbance at 280nm (E_{1%}^{1cm} 13.5).

40 Horseradish peroxidase labeled antibody was prepared using ImmunoPure Maleimide Activated Horseradish Peroxidase Kit (Pierce, Cat. 31494). Briefly, one mg of IgG was incubated with 80 µg of N-succinimidyl-S-acetylthioacetate for 30 min. After deacetylation with 5 mg of hydroxylamine HCl, modified IgG was separated by polyacrylamide desalting column. Protein pool mixed with one mg of maleimide activated horseradish peroxidase was incubated at room temperature for 1 hr.

ii) Quantitation of OCIF by sandwich EIA

45 Microtiter plates (Nunc MaxiSorp Immunoplate) were coated with rabbit anti-OCIF IgG by incubating 0.2 µg in 100 µl of 50 mM sodium bicarbonate buffer pH 9.6 at 4°C overnight. After blocking the plates by incubating for 1 hour at 37°C with 300 µl of 25% BlockAce/PBS (Snow Brand Milk Products), 100 µl of samples were incubated for 2 hours at room temperature. After washing the plates three times with PBST (PBS containing 0.05% Tween20), 100 µl of 1:10000 diluted horseradish peroxidase labeled anti-OCIF IgG was added and incubated for 2 hours at room temperature. The amount of OCIF was determined by incubation with 100 µl of a substrate solution (TMB, ScyTek Lab., Cat. TM4999) and measurement of the absorbance at 450 nm using an ImmunoReader (Nunc NJ2000). Purified recombinant OCIF was used as a standard protein and a typical standard curve was shown in Fig. 13.

EXAMPLE 25

Anti-OCIF monoclonal antibody

5 i) Preparation of hybridoma producing anti-OCIF monoclonal antibody.

OCIF was purified to homogeneity from culture medium of human fibroblasts, IMR-90 by the purification method described in Example 11. Purified OCIF was dissolved in PBS at a concentration of 10 µg/100 µl. BALB/c mice were immunized by administering this solution intraperitoneally three times every two weeks. In the first and the second
 10 immunizations, the emulsion composed of an equal volume of OCIF and Freund's complete adjuvant was administered. Three days after the final administration, the spleen was taken out, lymphocytes were isolated and fused with mouse myeloma p3x63-Ag8.653 cells according to the conventional method using polyethyleneglycol. Then the fused cells were cultured in HAT medium to select hybridoma. Subsequently, to check whether the selected hybridomas produce anti-OCIF antibody, anti-OCIF antibody in each culture medium of hybridomas was determined by solid phase ELISA which
 15 was prepared by coating each well in 96-well immunoplates (Nunc) with 100µl of purified OCIF (10µg/ml in 0.1 M NaHCO₃) and by blocking each well with 50% BlockAce (Snow Brand Milk Products Co. Ltd.). The hybridoma clones secreting anti-OCIF antibody were established by cloning 3 - 5 times by limit dilution and by screening using the above solid phase ELISA. Among thus obtained hybridoma clones, several hybridoma clones with high production of anti-OCIF antibody were selected.

20 ii) Production of anti-OCIF monoclonal antibodies.

Each hybridoma clone secreting anti-OCIF antibody, which was obtained in EXAMPLE 25-i), was transplanted intraperitoneally to mice given Pristane (Aldrich) at a cell density of 1×10^6 cells/mouse. The accumulated ascites was collected
 25 10 - 14 days after the transplantation and the ascites containing anti-OCIF specific monoclonal antibody of the present invention was obtained. Purified antibodies were obtained by Affigel protein A Sepharose chromatography (BioRad) according to the manufacturer's manual. That is, the ascites was diluted with equal volume of a binding buffer (BioRad) and applied to protein A column. The column was washed with a sufficient volume of the binding buffer and eluted with an elution buffer (BioRad). After neutralizing, the obtained eluate was dialyzed in water and subsequently lyophilized.
 30 The purity of the obtained antibody was analyzed by SDS/PAGE and a homogenous band with a molecular weight of about 150,000 was detected.

iii) Selection of monoclonal antibody having high affinity to OCIF

Each antibody obtained in EXAMPLE 25-ii) was dissolved in PBS and the concentration of protein in the solution was determined by the method of Lowry. Each antibody solution with the same concentration was prepared and then serially diluted with PBS. Monoclonal antibodies, which can recognize OCIF even at highly diluted solution, were selected by solid phase ELISA described in EXAMPLE 25-ii). Thus three monoclonal antibodies A1G5, E3H8 and D2F4 can be selected.

40 iv) Determination of class and subclass of antibodies

The class and subclass of the antibodies of the present invention obtained in EXAMPLE 25-iii) were analyzed using an immunoglobulin class and subclass analysis kit (Amersham). The procedure was carried out according to the protocol disclosed in the directions. The results were shown in Table 15. The antibodies of the present invention, E3H8, A1G5 and D2F4 belong to IgG₁, IgG_{2a} and IgG_{2b}, respectively.

Table 15

Analysis of class and subclass of the antibodies in the present invention.							
Antibody	IgG ₁	IgG _{2a}	IgG _{2b}	IgG ₃	IgA	IgM	κ
A1G5	-	+	-	-	-	-	+
E3H8	+	-	-	-	-	-	+
D2F4	-	-	+	-	-	-	+

v) Determination of OCIF by ELISA

Three kinds of monoclonal antibodies, A1G5, E3H8 and D2F4, which were obtained in EXAMPLE 25-iv), were used as solid phase antibodies and enzyme-labeled antibodies, respectively. Sandwich ELISA was constructed by each combination of solid phase antibody and labeled antibody. The labeled antibody was prepared using Immuno Pure Maleimide Activated Horseradish Peroxidase Kit (Pierce, Cat. No. 31494). Each monoclonal antibody was dissolved in 0.1 M NaHCO₃ at a concentration of 10 µg/ml, and 100 µl of the solution was added to each well in 96-well immunoplates (Nunc, MaxiSorp Cat. No. 442404) followed by allowing to stand at room temperature overnight. Subsequently, each well in the plates was blocked with 50% Blockace (Snow Brand Milk Products, Co., Ltd.) at room temperature for 50 minutes, and then was washed three times with PBS containing 0.1% Tween 20 (washing buffer).

A series of concentrations of OCIF was prepared by diluting OCIF with 1st reaction buffer (0.2 M Tris-HCl buffer, pH 7.4, containing 40% Blockace and 0.1% Tween 20). Each well in 96-well immunoplates was filled with 100 µl of the prepared OCIF solution with each concentration, allowed to stand at 37 °C for 3 hours, and subsequently washed three times with the washing buffer. For dilution of POD-labeled antibody, 2nd reaction buffer (0.1 M Tris-HCl buffer, pH 7.4, containing 25% Blockace and 0.1% Tween 20) was used. POD-labeled antibody was diluted 400-fold with 2nd reaction buffer, and 100 µl of the diluted solution was added to each well in the immunoplates. Each immunoplate was allowed to stand at 37 °C for 2 hours, and subsequently washed three times with the washing buffer. After washing, 100 µl of a substrate solution (0.1 M citrate-phosphate buffer, pH 4.5, containing 0.4 mg/ml of o-phenylenediamine HCl and 0.006% H₂O₂) was added to each well in the immunoplates and the immunoplates were incubated at 37°C for 15 min. The enzyme reaction was terminated by adding 50 µl of 6 N H₂SO₄ to each well. The optical density of each well was determined at 492 nm using an immunoreader (ImmunoReader NJ 2000, Nunc).

Using three kinds of monoclonal antibody in the present invention, each combination of solid phase and POD-labeled antibodies leads to a accurate determination of OCIF. Each monoclonal antibody in the present invention was confirmed to recognize a different epitope of OCIF. A typical standard curve of OCIF using a combination of solid phase antibody, A1G5 and POD-labeled antibody, E3H8 was shown in Fig. 14.

vi) Determination of OCIF in human serum

Concentration of OCIF in five samples of normal human serum was determined using an EIA system described in EXAMPLE 25-v). The immunoplates were coated with A1G5 as described in EXAMPLE 25-v), and 50 µl of 1st. reaction buffer was added to each well in the immunoplates. Subsequently, 50 µl of each human serum was added to each well in the immunoplates. The immunoplates were incubated at 37°C for 3 hours and then washed three times with the washing buffer. After washing, each well in the immunoplates was filled with 100 µl of POD-E3H8 antibody diluted 400-fold with 2nd. reaction buffer and incubated at 37°C for 2 hours. After washing the immunoplates three times with the washing buffer, 100 µl of the substrate solution described in EXAMPLE 25-v) was added to each well and incubated at 37°C for 15 min. The enzyme reaction was terminated by adding 50 µl of 6 N H₂SO₄ to each well in the immunoplates. The optical density of each well was determined at 492 nm using an immunoreader (ImmunoReader NJ 2000, Nunc). 1st. reaction buffer containing the known amount of OCIF was treated in the same way and a standard curve of OCIF as shown in fig. 2 was obtained. Using the standard curve of OCIF, the amount of OCIF in human serum sample was determined. The results were shown in Table 14.

Table 14

The amount of OCIF in normal human serum	
Serum Sample	OCIF Concentration (ng/ml)
1	5.0
2	2.0
3	1.0
4	3.0
5	1.5

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